



JOURNAL Patent: EP 1344834-A 557 17-SEP-2003;

F. HOFFMANN-LA ROCHE AG (CH)

## FEATURES

SOURCE

Location/Qualifiers  
1..3259  
/organism="Rattus norvegicus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10116"

## ORIGIN

Query Match 99.9%; Score 866; DB 6; Length 3259;

Best Local Similarity 100.0%; Pred. No. 3.1e-175;

Matches 866; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 362 CGTGAAGCGCTGCAAGCGGAGTCTGGGCTGCGAGAGCATGTCGCTCTCTGCTGAGG 421
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DB 841 TAGTGAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 866

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## RESULT 2

RNNGFR

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

RNNGFR 3259 bp mRNA linear ROD 21-MAR-1995  
Rat mRNA for fast nerve growth factor receptor (NGFR).  
X05137  
X05137.1 GI:56755  
nerve growth factor receptor.  
Rattus norvegicus (Norway rat)  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

SOURCE

1 (bases 1 to 3259)  
Radeke, M.J., Misko, T.P., Heu, C., Herzberg, J.A. and Shooter, E.M.  
Gene transfer and molecular cloning of the rat nerve growth factor  
receptor.  
Nature 325 (6105), 593-597 (1987)  
87115859  
3027580  
Data kindly reviewed (10-SEP-1987) by MISKO T.P.  
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/note="poc.N-linked glycosylation site"

## ORIGIN

Query Match 99.9%; Score 866; DB 10; Length 3259;

Best Local Similarity 100.0%; Pred. No. 3.1e-175;

Matches 866; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 CAGCTCCGCGGCGGAGCGGCTGAGACCGCATGGCAGTTTCAAGTCAAGCGAGACCATC 61
DB 1 CAGCTCCGCGGCGGAGCGGCTGAGACCGCATGGCAGTTTCAAGTCAAGCGAGACCATC 60
QY 62 GGTGCGGAGCGGAGCTAGCTAGAGAGCGGCTGACGCGGAGGCGGCTGCAATGAGA 121
DB 61 GGTGCGGAGCGGAGCTAGCTAGAGAGCGGCTGACGCGGAGGCGGCTGCAATGAGA 120
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DB 121 GGGCAGGTGCTGCTGCGAGCGCATGACCGGCTGCGCTCTGCTGCTGCTGCTAG 180
QY 182 GGGTGTCTCTGAGAGTGCAGAGAGACATGTTCCAGAGGCTGTACACCCAGCGGAG 241
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Qy      422 CAGACGATGACGTGTGACAGTGTGTCTATGTGTCTACTACAGACGAGACGAGTGTGCACT 481
Db      421 CAGACGATGACGTGTGACAGTGTGTCTATGTGTCTACTACAGACGAGACGAGTGTGCACT 480
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Db      481 GTGAGGCTGTGACGCGTGTGCGAGGTGGGCTGTGGGACTGTGTCTCTCTGCGAGCAAC 540
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Qy      602 ACCCGTGTCTACCTGTGACGCGTGTGCGAGGACACTGTGACGCGCACTTACGCGAGTGCAC 661
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Qy      662 CCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 721
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Qy      722 CGAGAGGCTGTGCGACGACGACGCGCCAGCAGCCAGGAGCTGTGTGTGTGTGTGTGTGTGT 781
Db      721 CGAGAGGCTGTGCGACGACGACGCGCCAGCAGCCAGGAGCTGTGTGTGTGTGTGTGTGT 780
Qy      782 ACCTTGTACCAAGTACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 841
Db      781 ACCTTGTACCAAGTACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
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Db      841 TAGTGACCGCGGCGGACGACCGGACGAC 866

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RESULT 3
BC038365      3441 bp      mRNA      linear      ROD 21-OCT-2003
LOCUS      Mus musculus nerve growth factor receptor (TNFR superfamily, member
DEFINITION      16), mRNA (cdna clone MGC:35588 IMAGE:5367638), complete cds.
ACCESSION      BC038365
VERSION      BC038365.1 GI:23468246
KEYWORDS      MGC.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3441)
Strusberg,R.L., Fengold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,S.F., Collins,F.S., Wagner,L., Shermen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhac,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Ditschenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Schaefer,T.E., Brownstein,W.J., Usdin,T.B., Toshiyuki,S.,
Carrinci,P., Prange,C., Rana,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullany,S.J., Bosak,S.A., McSwain,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahy,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,
Sanchéz,A., Whitting,M., Madan,A., Young,A.C., Rodriguez,S.,
Boutard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalek,U., Smalins,D.E.,

```

# TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL

Schmerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

2 (bases 1 to 3441)

Strusberg,R.  
 Direct Submission  
 Submitted (01-OCT-2002) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>

Contract: MGC help desk  
 Email: [cgabs-rt@mail.nih.gov](mailto:cgabs-rt@mail.nih.gov)  
 Tissue Procurement: The Cepko Laboratory  
 cDNA Library preparation: Life Technologies, Inc.  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LINL)  
 Sequencing Center  
 Center code: BCM-HGSC  
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
 Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louieged, H.,  
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nantavati,  
 A.N., Gibbs, R.A.

## REMARK COMMENT

Clone distribution: MGC clone distribution information can be found  
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 This clone was selected for full length sequencing because it  
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 Location/Qualifiers

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misc\_feature  
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 Some (but not all) of these domains form homotypic and



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Oy	651	CGAGTGCACGCCCTGGGCTGTGTCTGAATGCGAACAGATCCCTGGTTCATGGATCCCAAG	710
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Oy	711	GTCTACGCCCCCGGAGGGGCTCCGACAGACAGCGGCCGACACCACGAGAGCCGTAAGTCC	770
Db	601	GTCTACGCCCCCGGAGGGGCTCTGACGTCTCAACATCCACAGCATCCAGAGGCCGAGAGCAC	660
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VERSION	A43530.1	GI:2298718	

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unidentified	unidentified	1 (bases 1 to 1600)	Bordignon, C. and Murraro, F.	METHOD OF MARKING EUKARYOTIC CELLS BY THE USE OF A CELL SURFACE RECEPTOR AS A MARKER	Patent: WO 9506723-A 1 09-MAR-1995;	
			BOEHRINGER MANNHEIM GMBH (DE)		Other publication IT 1261847 960603	
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Quer

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Best Local Similarity	85.0%;	Pred. No. 1.7e-124;		
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QY 86 AAGCGGAGCGCTGACGCCCGGAGCGCTGCAATGAGGAGGCGCAGATGTGCTCTCAGCGCA 145

Db 85 AACTCGAGCGCTGCGCGGAGGCGGGC---GATGGGGGCAAGTGTCCACCGGCGCGGCCA 141

QY 146 TGAACCGGCTGGCGCCCTGCTGCTGCTGCTGCTAATTCATAGGGGTGTGCTCTGAGAGTGCAGG 205

Db 142 TGACCGGGCGCGCCCTGCTGCTGTCTGTCTGTCTGTGGGGGTGTCTTGTGAAGTTCACAG 201

QY 206 AGACATGTTCCACAGGCTGTGTACCCACAGCGGAGAGTGTCTGCAAAGCTTCAACTTGG 265

Db 202 AGGCATGCCCCACAGGCTGTATCACACACAGCGGTAGTGTCCAAAGCTTGCAACTTGG 261

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DEFINITION	Sequence 1 from patent US 6074836.	linear
ACCESSION	AR098123	PAT 14-FEB-2001
VERSION	AR098123.1	GI:12807380

ORGANISM

Unclassified.  
1 (bases 1 to 1600)

**AUTHORS** Bordignon, C. and Mavillo, F.  
**TITLE** Method of marking eukaryotic cells  
**JOURNAL** Patent: US 6074836-A 1 13-JUN-2000;

FEATURES	Location/Qualifiers
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ORIGIN

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Matches 716;	Conservative	0;	Mismatches 123;	Indels 3;
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[illegible][illegible]

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 12, 2004, 16:27:22 ; Search time 21 seconds  
(without alignments)  
1149.718 Million cell updates/sec

Title: US-09-821-831-4

Sequence: 1 MRBAGACSMDBRLRLILL.....MTTVMSSQPVYRTGTDN 251

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 28366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 28366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1387	100.0	425	1 A26431	nerve growth facto
2	1244	89.7	427	1 GQHUN	nerve growth facto
3	883.5	63.7	416	1 JN0006	nerve growth facto
4	215.5	15.5	461	1 GQRTT1	tumor necrosis fac
5	204	15.4	277	2 I37552	OX40 homolog - hum
6	202	14.6	305	2 A46476	B cell-associated
7	197.5	14.2	454	1 GQMT1	tumor necrosis fac
8	196.5	14.2	325	1 B43692	tumor necrosis fac
9	193.5	14.0	326	1 GQVZML	T2 protein - myxom
10	189.5	13.7	271	2 SI2783	OX40 antigen precu
11	186.5	13.4	272	2 I48700	gene OX40 protein
12	182.5	13.2	459	2 I48854	gene murine tumor
13	180.5	13.0	474	2 B38634	tumor necrosis fac
14	178	12.8	651	2 UC7705	death receptor-6 -
15	175.5	12.7	277	2 A60771	B-cell activation
16	175.5	12.6	435	2 S14482	tumor necrosis fac
17	171.5	12.4	3075	2 S14458	laminin alpha-1 ch
18	171.5	12.3	461	1 UC4302	tumor necrosis fac
19	170.5	12.3	461	1 A35356	tumor necrosis fac
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21	161.5	11.6	493	2 UC3486	membrane glycopro
22	159.5	11.5	314	2 I37383	PAS soluble protei
23	158	11.4	557	2 A48434	variant-specific s
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30	148	10.7	255	2 I38426	lymphocyte activat
31	143.5	10.3	677	2 C42125	trophozoite cystei
32	142.5	10.3	3712	2 S18253	laminin alpha-1 ch
33	142	10.2	1274	2 T42017	cysteine rich prot
34	141	10.2	348	2 T28622	hypothetical prote
35	141	10.2	349	2 D36858	gene G4R protein -
36	139	10.0	349	2 D72175	G2R protein - vari
37	139	10.0	3635	2 T10053	laminin alpha 5 ch
38	137.5	9.9	1372	2 T25933	hypothetical prote
39	137	9.9	3084	1 M44517	laminin alpha-1 ch
40	136.5	9.8	260	1 A46517	CD27 antigen precu
41	136.5	9.8	1187	2 T18355	hypothetical prote
42	136	9.8	962	2 UC5871	subtilisin-like pr
43	136	9.8	975	2 UC5570	subtilisin-like pr
44	134.5	9.7	354	2 T22274	hypothetical prote
45	134.5	9.7	3707	2 S18252	heparan sulfate pr

## ALIGNMENTS

RESULT 1  
A26431  
nerve growth factor receptor precursor, low affinity - rat  
N/Alternate names: NGF receptor  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C/Accession: A26431; PH1229  
R/RefSeq: M. J. Misko, T. P. Hsu, C. J. Herzberg, L. A. Shooter, E. M.  
Nature 325, 593-597, 1987  
A/Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.  
A/Reference number: A26431; PMID:87115859; PMID:3027580  
A/Accession: A26431  
A/Molecule type: mRNA  
A/Residues: 1-425 <RAD>  
A/Cross-references: GB:X05137; NID:956755; PIDN:CA28783.1; PID:956756  
R/Metals: M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.  
Gene 121, 247-254, 1992  
A/Title: Regulatory elements and transcriptional regulation by testosterone and retinoic  
A/Reference number: PH1229; PMID:93077038; PMID:1446821  
A/Accession: PH1229  
A/Molecule type: DNA  
A/Residues: 1-20 <MET>  
A/Cross-references: GB:X61265  
A/Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma  
C/Comment: The cysteine-rich region of the extracellular domain may form part or all of  
C/Comment: this protein is thought to form a high-affinity receptor when it associates w  
C/Genetics:  
A/Intons: 20/3  
C/Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
C/Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t  
F.1.29/Domin: signal sequence #status predicted <SIS>  
F.30-251/Product: nerve growth factor receptor #status predicted <EXT>  
F.30-251/Domin: extracellular #status predicted <EXT>  
F.33-66/Domin: NGF receptor repeat homology <NG3>  
F.68-109/Domin: NGF receptor repeat homology <NG3>  
F.110-148/Domin: NGF receptor repeat homology <NG3>  
F.150-190/Domin: NGF receptor repeat homology <NG4>  
F.198-249/Region: serine/threonine-rich  
F.252-273/Domin: transmembrane #status predicted <MEM>  
F.274-425/Domin: intracellular #status predicted <INT>  
F.61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 1387; DB 1; Length 425;  
Best Local Similarity 100.0%; Pred. No. 6.5e-90; Indels 0; Gaps 0;  
Matches 251; Conservative 0; Mismatches 0;

QY 1 MRBAGACSMDBRLRLILLIGVSSGAKETSTGYTHSGCCACNLGEGVAPCGA 60  
DB 1 MRBAGACSMDBRLRLILLIGVSSGAKETSTGYTHSGCCACNLGEGVAPCGA 60  
QY 61 NOTVCEPCLDNVTFSDVSAATEPCKPTECLGTQSNASAPCEVADDAVCACAYYQDEET 120

Db 61 NOTVCEPLDNTVTSDDVSAATEPCCTCECLGLQSMNAPCEVADDAVCAVCATGYDDEET 120  
 QY 121 GHCEACSVCEVGGGLVFSQCDKONTVCCECEEGTYSDEANHVDPCLPCTVCEDTERQLE 180  
 Db 121 GHCEACSVCEVGGGLVFSQCDKONTVCCECEEGTYSDEANHVDPCLPCTVCEDTERQLE 180  
 QY 181 CTNPADACEEIPGRMIPRSTPEPGSDSTAPSTQCEPVEPEODLVPTVADMTVTMGSS 240  
 Db 181 CTNPADACEEIPGRMIPRSTPEPGSDSTAPSTQCEPVEPEODLVPTVADMTVTMGSS 240  
 QY 241 QPVVTRGTTDN 251  
 Db 241 QPVVTRGTTDN 251  
 RESULT 2  
 GORUN  
 nerve growth factor receptor precursor, low affinity [validated] - human  
 N/Alternate names: NGF receptor  
 C/Species: Homo sapiens (man)  
 C/Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text\_change 08-Dec-2000  
 C/Accession: A25218; A60204; S21689; I57638  
 R/Johnson, D.; Lanthan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.  
 Cell 47, 545-554, 1986  
 A/Title: Expression and structure of the human NGF receptor.  
 A/Reference number: A25218; PMID:87051725; PMID:3022937  
 A/Accession: A25218  
 A/Molecule type: mRNA  
 A/Residues: 1-427 <JOH>  
 A/Cross-references: GB:M4764; NID:G189204; PIDN:AA59544.1; PID:G189205  
 R/Marano, N.; Dietzschold, B.; Farley Jr., J.J.; Schacteman, G.; Thompson, S.; Grob, P.;  
 J. Neurochem. 48, 225-232, 1987  
 A/Title: Purification and amino terminal sequencing of human melanoma nerve growth factor  
 A/Reference number: A60204; PMID:87085574; PMID:3025363  
 A/Accession: A60204  
 A/Molecule type: protein  
 A/Residues: 29-31, 'T', '33-42', 'TT', '45-46', 'TX', '50-51', 'XX', '54-56 <MAR>  
 A/Experimental source: melanoma cell line A875  
 A/Note: This sequence has been corrected by a note added in proof to follow the nucleoti  
 R/Vissavajjala, P.; Leszyk, J.D.; Lin-Goske, J.; Ross, A.H.  
 Arch. Biochem. Biophys. 294, 244-252, 1992  
 A/Title: Structural domains of the extracellular domain of human nerve growth factor rec  
 A/Reference number: S21689; PMID:92196017; PMID:1372432  
 A/Accession: S21689  
 A/Status: preliminary  
 A/Residues: 183-208 <VIS>  
 R/Sehgal, A.; Patel, N.; Chao, M.  
 Mol. Cell. Biol. 8, 3160-3167, 1988  
 A/Title: A constitutive promoter directs expression of the nerve growth factor receptor  
 A/Reference number: I57638; PMID:89096903; PMID:2850461  
 A/Accession: I57638  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-22 <RES>  
 A/Cross-references: M21621; NID:G189206; PIDN:AA36363.1; PID:G189207  
 C/Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma  
 C/Comment: The cysteine-rich region of the extracellular domain may form part or all of  
 C/Comment: This protein is thought to form a high-affinity receptor when it associates w  
 C/Comment: This receptor undergoes both N- and O-linked glycosylation.  
 C/Genetics:  
 A/Gene: GDB:NGFR  
 A/Cross-references: GDB:120234; OMTM:162010  
 A/Map position: 17q21-17q22  
 C/Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
 C/Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t  
 F1-29/Dominant: signal sequence #status predicted <SIG>  
 F1-29-427/Product: nerve growth factor receptor #status experimental <MAT>  
 F1-29-250/Dominant: extracellular #status predicted <EXT>  
 F1-29-65/Dominant: NGF receptor repeat homology <NG1>  
 F1-67-108/Dominant: NGF receptor repeat homology <NG2>  
 F1-109-147/Dominant: NGF receptor repeat homology <NG3>  
 F1-149-189/Dominant: NGF receptor repeat homology <NG4>

F1-197-248/Region: serine/threonine-rich  
 F1-251-272/Dominant: transmembrane #status predicted <TRM>  
 F1-273-427/Dominant: intracellular #status predicted <INT>  
 F1-60/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 89.7%; Score 1244; DB 1; Length 427;  
 Best Local Similarity 90.7%; Pred. No. 6, 4e-80;  
 Matches 225; Conservative 6; Mismatches 17; Indels 0; Gaps 0;  
 QY 4 AGAAGSAMRLLILLILLIGVSGGAKETQSLGTYHSGECCRAKNGLEGVAQPGCANQT 63  
 Db 3 AGATGRAMDPRILLILLIGVSLGAKEXAPGTYHSGECCRAKNGLEGVAQPGCANQT 62  
 QY 64 VCEPCLDNTVTSDDVSAATEPCCTCECLGLQSMNAPCEVADDAVCAVCATGYDDEET 123  
 Db 63 VCEPCLDNTVTSDDVSAATEPCCTCECLGLQSMNAPCEVADDAVCAVCATGYDDEET 122  
 QY 124 EACVCEVGGGLVFSQCDKONTVCCECEEGTYSDEANHVDPCLPCTVCEDTERQLE 183  
 Db 123 EACVCEVGGGLVFSQCDKONTVCCECEEGTYSDEANHVDPCLPCTVCEDTERQLE 182  
 QY 184 WADACEEIPGRMIPRSTPEPGSDSTAPSTQCEPVEPEODLVPTVADMTVTMGSSQPV 243  
 Db 183 WADACEEIPGRMIPRSTPEPGSDSTAPSTQCEPVEPEODLVPTVADMTVTMGSSQPV 242  
 QY 244 VTRGTTDN 251  
 Db 243 VTRGTTDN 250  
 RESULT 3  
 JN0006  
 nerve growth factor receptor, low affinity precursor - chicken  
 N/Alternate names: NGF receptor  
 C/Species: Gallus gallus (chicken)  
 C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C/Accession: JN0006; A60504  
 R/Larage, T.H.; Weiskamp, G.; Heider, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reic  
 Neuron 2, 1123-1134, 1989  
 A/Title: Structure and developmental expression of the nerve growth factor receptor in t  
 A/Reference number: JN0006; PMID:9016579; PMID:2860385  
 A/Accession: JN0006  
 A/Molecule type: mRNA  
 A/Residues: 1-416 <LAR>  
 A/Experimental source: embryonic chick brain  
 R/Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, E.F.; Bothwell, M.  
 Dev. Biol. 137, 287-304, 1990  
 A/Title: Structure and developmental expression of the chicken NGF receptor.  
 A/Reference number: A60504; PMID:90152140; PMID:2154393  
 A/Accession: A60504  
 A/Status: preliminary; not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 21-35, 'V', '37-172', 'K', '174-275', 'S', '277-395', 'R', '397-416 <HEU>  
 C/Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma  
 C/Comment: The cysteine-rich region of the extracellular domain may form part or all of  
 C/Comment: This protein is thought to form a high-affinity receptor when it associates v  
 C/Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
 C/Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t  
 F1-20/Dominant: signal sequence #status predicted <SIG>  
 F1-21-416/Product: nerve growth factor receptor #status predicted <MAT>  
 F1-21-416/Product: nerve growth factor receptor #status predicted <EXT>  
 F1-24-57/Dominant: NGF receptor repeat homology <NG1>  
 F1-59-100/Dominant: NGF receptor repeat homology <NG2>  
 F1-101-139/Dominant: NGF receptor repeat homology <NG3>  
 F1-141-181/Dominant: NGF receptor repeat homology <NG4>  
 F1-189-237/Region: serine/threonine-rich  
 F1-240-261/Dominant: transmembrane #status predicted <TRM>  
 F1-262-416/Dominant: intracellular #status predicted <INT>  
 F1-52/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 63.7%; Score 893.5; DB 1; Length 416;  
 Best Local Similarity 66.1%; Pred. No. 9, 7e-55;  
 Matches 156; Conservative 33; Mismatches 44; Indels 3; Gaps 1;







modulate cell survival by antagonising the death signalling region or promoting apoptosis by providing cells with the genetic material to express the death signalling region adjacent, proximal, or otherwise juxtaposed or associated membrane of a cell or to express the death signalling region in multicentric form. The polypeptides and methods of the invention are useful for inhibiting, reducing or antagonizing p75-NTR-mediated death signals in neural cells. In particular, the methods are used for the treatment or prophylaxis of disease conditions associated with neural death or where cell death is to be promoted such as in treating or preventing cancer growth and/or development. Other diseases capable of treatment include neurodegenerative diseases, such as cerebral palsy, trauma induced paralysis, vascular ischemia associated with stroke, neural tumors, motorneurone disease, Parkinson's disease, Huntington's disease, Alzheimer's disease, multiple sclerosis and peripheral neuropathies associated with diabetes, heavy metal or alcohol toxicity, renal failure, and/or infectious diseases such as Herpes, rubella, measles, chicken pox, HIV and HTLV-1 (all claimed). The methods are also useful for treating neurons or glia damaged by trauma or disease (claimed). Animals which can be treated include humans, livestock animals, laboratory test animals, companion animals, and captive wild animals

Sequence 3260 BP; 718 A; 976 C; 913 G; 653 T; 0 U; 0 Other;

Query Match 100.0%; Score 867; DB 3; Length 3260;  
Best Local Similarity 100.0%; Pred. No. 7.9e-215;  
Matches 867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ACAGCTCCGCGGCGGAGCAGCGGCTGGAGCCGATCGAGCTCAGCCAGACCAT 60  
1 ACAGCTCCGCGGCGGAGCAGCGGCTGGAGCCGATCGAGCTCAGCCAGACCAT 60  
61 CGGTCGCGGAGCGGAGCTGAGTAAGCGGAGCGGCTGAGCGGAGCGGCTGAGG 120  
61 CGGTCGCGGAGCGGAGCTGAGTAAGCGGAGCGGCTGAGCGGAGCGGCTGAGG 120  
121 AAGGAGCGGCTGCGCTGCGAGCGGCGGATGAGCGGCTGCGCTGCGTGTGTTTGA 180  
121 AAGGAGCGGCTGCGCTGCGAGCGGCGGATGAGCGGCTGCGCTGCGTGTGTTTGA 180  
121 AAGGAGCGGCTGCGCTGCGAGCGGCGGATGAGCGGCTGCGCTGCGTGTGTTTGA 180  
181 GGGGTCCTCTGAGAGTGCAGAGGAGCATTTTCCAGAGCGGCTGAGCGGAGCGG 240  
181 GGGGTCCTCTGAGAGTGCAGAGGAGCATTTTCCAGAGCGGCTGAGCGGAGCGG 240  
181 GGGGTCCTCTGAGAGTGCAGAGGAGCATTTTCCAGAGCGGCTGAGCGGAGCGG 240  
241 GAGTGTGCGAAGCGCTGCGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300  
241 GAGTGTGCGAAGCGCTGCGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300  
241 GAGTGTGCGAAGCGCTGCGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300  
301 ACCGTCGTGGAACCGCTGCGAAGCATTTTCCAGATGAGTGTGAGCGGCGGCGG 360  
301 ACCGTCGTGGAACCGCTGCGAAGCATTTTCCAGATGAGTGTGAGCGGCGGCGG 360  
301 ACCGTCGTGGAACCGCTGCGAAGCATTTTCCAGATGAGTGTGAGCGGCGGCGG 360  
361 CGGTGGAAGCGCTGCGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420  
361 CGGTGGAAGCGCTGCGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420  
361 CGGTGGAAGCGCTGCGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420  
421 GCAGAGTGTGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGT 480  
421 GCAGAGTGTGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGT 480  
421 GCAGAGTGTGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGT 480  
481 TGTGAGGCTTGTGAGCGGCTGCGAGGCTGCGAGCTGCTGCTGCTGCGAGAGCAA 540  
481 TGTGAGGCTTGTGAGCGGCTGCGAGGCTGCGAGCTGCTGCTGCTGCGAGAGCAA 540  
481 TGTGAGGCTTGTGAGCGGCTGCGAGGCTGCGAGCTGCTGCTGCTGCGAGAGCAA 540  
541 CAGAGACAGTGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGT 600  
541 CAGAGACAGTGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGT 600  
541 CAGAGACAGTGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGT 600  
601 GACCCGTGCTTACCTGCGAGCGGTGTGCGAGGAGCATGAGCGGCGGAGTTACGCA 660  
601 GACCCGTGCTTACCTGCGAGCGGTGTGCGAGGAGCATGAGCGGCGGAGTTACGCA 660  
601 GACCCGTGCTTACCTGCGAGCGGTGTGCGAGGAGCATGAGCGGCGGAGTTACGCA 660  
661 CCTGGGCTGATGCTGATGATGCGAAGAGATCCCTGATGATGATGATGATGATG 720  
661 CCTGGGCTGATGCTGATGATGCGAAGAGATCCCTGATGATGATGATGATGATG 720

DB 661 CCTGGGCTGATGCTGATGATGCGAAGAGATCCCTGATGATGATGATGATGATG 720  
QY 721 CCGAGAGGCTTCCGAGAGCAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780  
DB 721 CCGAGAGGCTTCCGAGAGCAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780  
QY 781 GACCTGTATCCAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 840  
DB 781 GACCTGTATCCAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 840  
QY 841 GTTGTATCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 867  
DB 841 GTTGTATCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 867

RESULT 3

ADB58069 standard; DNA; 3259 BP.

ADB58069;

04-DEC-2003 (first entry)

Toxicity-related gene, SEQ ID 3095.

Toxic; toxin; gene expression profile; hepatotoxicity; liver; drug screening; toxicity assay; ds.

Unidentified.

W02003064624-A2.

07-AUG-2003.

31-JAN-2003; 2003WO-US003194.

31-JAN-2002; 2002US-00060087.

15-MAR-2002; 2002US-0364045P.

15-MAR-2002; 2002US-0364055P.

30-DEC-2002; 2002US-0436643P.

(GENE-) GENE LOGIC INC.

Mendrick D, Porter M, Johnson K, Higgs B, Caastle A, Blashoff M;

WPI; 2003-689530/65.

Predicting a toxic effect of a compound, useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays, PT comprises preparing gene expression profile of tissue or cells exposed to the compound.

Claim 1; SEQ ID NO 3095; 1156BP; English.

The present invention relates to a method for predicting a toxic effect of a compound. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising SEQ ID 1-4925, where differential expression of the gene indicates at least one toxic effect. The method is useful for predicting or the progression of a toxic effect of a compound, predicting hepatotoxicity or the progression of a toxic effect of a compound, identifying an agent that modulates the onset or progression of a toxic response, predicting the cellular pathways that a compound modulates in a cell, and identifying an agent that modulates at least one activity of a protein. The method and compositions of the present invention using a database of genes having liver toxin-induced differential expression, are useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pcl\_sequences.





RESULT 6  
 ID AB235044  
 AB235044 standard, cDNA; 3386 BP.  
 AC AB235044;  
 XX  
 DT 05-FEB-2003 (first entry)  
 XX  
 DE Human gene expression profile polynucleotide SEQ ID NO 156.  
 XX  
 KM Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;  
 KM bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;  
 KM tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;  
 KM gene expression; gene; ss.  
 XX  
 OS Homo sapiens.  
 PN WO200274979-A2.  
 XX  
 PD 26-SEP-2002.  
 XX  
 PF 20-MAR-2002; 2002MO-US008456.  
 XX  
 PR 20-MAR-2001; 2001US-0276947P.  
 XX  
 PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  
 XX  
 PI Wan J, Wang Y;  
 DR WPI; 2002-740862/80.  
 XX  
 PT New gene expression profile generated from primary, endothelial,  
 PT epithelial, and muscle cell types, useful for identifying disease  
 PT pathologies involving alterations of gene expression, e.g. cancer.  
 PS  
 PS Claim 3; Page 380-381, 850pp; English.  
 XX  
 CC The invention relates to a gene expression profile comprising one or more  
 CC Genes (AB235889-AB235692) and generated from a cell type. The cell type  
 CC is a coronary artery endothelium, umbilical artery or vein endothelium,  
 CC aortic endothelium, dermal microvascular endothelium, pulmonary artery  
 CC endothelium, myometrium microvascular endothelium, keratinocyte  
 CC epithelium, bronchial epithelium, mammary epithelium, prostate  
 CC epithelium, renal cortical epithelium, renal proximal tubule epithelium,  
 CC small airway epithelium, renal epithelium, umbilical artery smooth  
 CC muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle,

Db 742 CCAGCACCCAGAGCCTGAGGCACCTCCAGAACAGACCTATAGCCAGCACGGTGCAG 80



FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: one-of(1512)  
 OTHER INFORMATION: /function="Sacti cleavage site"

Query Match 72.6%; Score 629.2; DB 3; Length 1600;  
 Best Local Similarity 85.0%; Pred. No. 2,9e-152;  
 Matches 716; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

26 GGAAGCGATGCGAGTTCAGCTCAGCGGACCAATGAGTGTGCGAGCGGAGTGAAGCTAG 85  
 25 GGGGGGGCGCTGAGACGCGAGCGAGCGGACCCATCATGTCGCAAGCGGAGCGAGCTGG 84  
 86 AAGCGAGCGGCTGACGCGGAGCGGCTGCAATGAGAGGAGGAGTGTGCTGCTGAGCGGCA 145  
 85 AAGTCGAGCGGCTGCGCGGAGGAGCGGCGC--GATGGGGGAGGTGCGACCGCGCGCA 141  
 146 TGAACCGGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 205  
 142 TGAACCGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 201  
 206 AGACATGCTCCACAGCGGCTGACACCCAGCGGAGAGTGTGCGAGCGGAGCTGCAACTGG 265  
 202 AGGATGCGCCGACAGCGGCTGACACACAGCGGAGTGTGCGAGCGGAGCTGCAACTGG 261  
 266 GCGAAGCGGCTGAGCGGCTGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 325  
 262 GCGAGGCTGAGCGGCTGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 321  
 326 ATGTTACATCTCCGATGCTGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 385  
 322 GCGTGAAGTCTCCGAGTGTGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 381  
 386 TGGGCTGCGAGCGATGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 445  
 382 TGGGCTGCGAGCGATGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 441  
 446 CCTATGCTACTACAGAGCGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 505  
 442 CCTAGCGCTACTACAGAGCGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 501  
 506 TGGGCTGCGAGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 565  
 502 GCGGCTGCGAGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 561  
 566 CAGAGCGGAGCGATGCTGCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 625  
 562 CCGAGCGGAGCGATGCTGCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 621  
 626 GCGAGGAGCGATGCTGCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 685  
 622 GCGAGGAGCGATGCTGCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 681  
 686 AGATGCGCTGCGAGCGATGCTGCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 745  
 682 AGATGCGCTGCGAGCGATGCTGCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 741  
 746 CCGAGCGGAGCGATGCTGCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 805  
 742 CCGAGCGGAGCGATGCTGCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 801  
 806 ATATGCTGAGCGATGCTGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 865  
 802 CTGCTGCTGAGCGATGCTGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 861  
 866 AC 867  
 862 AC 863

RESULT 2  
 US-09-041-886-1

Sequence 1, Application US/09041886  
 Patent No. 6235872  
 GENERAL INFORMATION:  
 APPLICANT: Bredesen, Dale E.  
 APPLICANT: Rabizadeh, Sharoz  
 TITLE OF INVENTION: Prepropeptide peptides, dependence  
 TITLE OF INVENTION: Polypeptides and methods of use  
 NUMBER OF SEQUENCES: 72  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Campbell & Flores LLP  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTRY: United States  
 ZIP: 92122  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/041,886  
 FILING DATE:  
 CLASSIFICATION:  
 ATORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-LJ 2626  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 535-9001  
 TELEFAX: (619) 535-8949  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3386 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 114..1395  
 US-09-041-886-1

Query Match 72.6%; Score 629.2; DB 3; Length 3386;  
 Best Local Similarity 85.0%; Pred. No. 3.5e-152;  
 Matches 716; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

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 25 GGGGGGGCGCTGAGACGCGAGCGGAGCGGACCCATCATGTCGCAAGCGGAGCGAGCTGG 84  
 86 AAGCGAGCGGCTGACGCGGAGCGGCTGCAATGAGAGGAGGAGTGTGCTGCTGAGCGGCA 145  
 85 AAGTCGAGCGGCTGCGCGGAGGAGCGGCGC--GATGGGGGAGGTGCGACCGCGCGCA 141  
 146 TGAACCGGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 205  
 142 TGAACCGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 201  
 206 AGACATGCTCCACAGCGGCTGACACCCAGCGGAGAGTGTGCGAGCGGAGCTGCAACTGG 265  
 202 AGGATGCGCCGACAGCGGCTGACACACAGCGGAGTGTGCGAGCGGAGCTGCAACTGG 261  
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 326 ATGTTACATCTCCGATGCTGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 385  
 322 GCGTGAAGTCTCCGAGTGTGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 381  
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Matches 867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ACAGCTCCGCGGCGGAGAGGCGCTTGAGAGCGCATGCGAGTTCAAGTTCAGCGGAGACCAT 60

QY 61 CGGTCTGCGGAGCGGAGCTAGAGTGAAGCGGAGCGCTGACCGCGGAGCGTGCATATGAG 120

DB 61 CGGTCTGCGGAGCGGAGCTAGAGTGAAGCGGAGCGCTGACCGCGGAGCGTGCATATGAG 120

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DB 121 AGGCGAGGTGTCTGCTGCGAGCGGAGTGAAGCGGAGCGCTGCTGCTGCTGCTGCTGCTG 180

QY 181 GGGGTGTCTGCTGAGGTGCGAAGAGAGATGTTCCAGAGGCTGTACACCCACAGCGGA 240

DB 181 GGGGTGTCTGCTGAGGTGCGAAGAGAGATGTTCCAGAGGCTGTACACCCACAGCGGA 240

QY 241 GAGTGTGCGAAGCGCTGCAACTTGGGCGAAGGCGTGGCCAGCCCTGGGAGCCCAACGAG 300

DB 241 GAGTGTGCGAAGCGCTGCAACTTGGGCGAAGGCGTGGCCAGCCCTGGGAGCCCAACGAG 300

QY 301 ACCGTGTGGAACCTGCTGCGAACAATGTTACATTTCCGAGTGTGAGCGCCACTGAG 360

DB 301 ACCGTGTGGAACCTGCTGCGAACAATGTTACATTTCCGAGTGTGAGCGCCACTGAG 360

QY 361 CGGTGCAAGCGGAGCGGAGTGCCTGCGGAGTGCAGAGCATGCTGCTGCTGCTGCTGCTG 420

DB 361 CGGTGCAAGCGGAGCGGAGTGCCTGCGGAGTGCAGAGCATGCTGCTGCTGCTGCTGCTG 420

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QY 481 TGTGAGGCTTGCAGCGTGTGCGAGTGTGCTTATGCTTACAGAGAGAGAGAGACTGGCCAC 540

DB 481 TGTGAGGCTTGCAGCGTGTGCGAGTGTGCTTATGCTTACAGAGAGAGAGAGACTGGCCAC 540

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QY 601 GAGCCGCTGCTTACCTGCGAGCGTGTGCGAGGAGACACTGAGCGGAGTTCAGAGTGCAG 660

DB 601 GAGCCGCTGCTTACCTGCGAGCGTGTGCGAGGAGACACTGAGCGGAGTTCAGAGTGCAG 660

QY 661 CCCTGCGGCTGATGCTGATGCGAAGAGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 720

DB 661 CCCTGCGGCTGATGCTGATGCGAAGAGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 720

QY 721 CCGGAGGCGCTGCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 780

DB 721 CCGGAGGCGCTGCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 780

QY 781 GACCTGTGACCGAGTACAGTGTGCGAGTGTGCTGATGCTGATGCGAGTGTGCTGCTGCTG 840

DB 781 GACCTGTGACCGAGTACAGTGTGCGAGTGTGCTGATGCTGATGCGAGTGTGCTGCTGCTG 840

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DB 841 GTAGTGAACCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 867

APPLICANT: Surinder, Cheema

TITLE OF INVENTION: Method of Modularizing Cell Survival and

FILE REFERENCE: 3206,1001-000

CURRENT APPLICATION NUMBER: US/09/821,831

PRIOR FILING DATE: 1999-10-07

PRIOR APPLICATION NUMBER: PCT/AU99/00860

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: AU PQ0701

PRIOR FILING DATE: 1999-06-01

PRIOR APPLICATION NUMBER: AU PP6351

PRIOR FILING DATE: 1998-10-07

PRIOR APPLICATION NUMBER: AU PP6353

PRIOR FILING DATE: 1998-10-06

NUMBER OF SEQ ID NOS: 72

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 3260

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic CDNA Sequence of Human

NAME/KEY: CDS

LOCATION: (115)...(1389)

US-09-821-831-1

Query Match 100.0%; Score 867; DB 9; Length 3260;

Best Local Similarity 100.0%; Pred. No. 4,8e-237;

Matches 867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ACAGCTCCGCGGCGGAGAGGCGCTTGAGAGCGCATGCGAGTTCAAGTTCAGCGGAGACCAT 60

QY 61 CGGTCTGCGGAGCGGAGCTAGAGTGAAGCGGAGCGCTGACCGCGGAGCGTGCATATGAG 120

DB 61 CGGTCTGCGGAGCGGAGCTAGAGTGAAGCGGAGCGCTGACCGCGGAGCGTGCATATGAG 120

QY 121 AGGCGAGGTGTCTGCTGCGAGCGGAGTGAAGCGGAGCGCTGCTGCTGCTGCTGCTGCTG 180

DB 121 AGGCGAGGTGTCTGCTGCGAGCGGAGTGAAGCGGAGCGCTGCTGCTGCTGCTGCTGCTG 180

QY 181 GGGGTGTCTGCTGAGGTGCGAAGAGAGATGTTCCAGAGGCTGTACACCCACAGCGGA 240

DB 181 GGGGTGTCTGCTGAGGTGCGAAGAGAGATGTTCCAGAGGCTGTACACCCACAGCGGA 240

QY 241 GAGTGTGCGAAGCGCTGCAACTTGGGCGAAGGCGTGGCCAGCCCTGGGAGCCCAACGAG 300

DB 241 GAGTGTGCGAAGCGCTGCAACTTGGGCGAAGGCGTGGCCAGCCCTGGGAGCCCAACGAG 300

QY 301 ACCGTGTGGAACCTGCTGCGAACAATGTTACATTTCCGAGTGTGAGCGCCACTGAG 360

DB 301 ACCGTGTGGAACCTGCTGCGAACAATGTTACATTTCCGAGTGTGAGCGCCACTGAG 360

QY 361 CGGTGCAAGCGGAGCGGAGTGCCTGCGGAGTGCAGAGCATGCTGCTGCTGCTGCTGCTG 420

DB 361 CGGTGCAAGCGGAGCGGAGTGCCTGCGGAGTGCAGAGCATGCTGCTGCTGCTGCTGCTG 420

QY 421 GCAGAGATGAGTGTGCGAGTGTGCTTATGCTTACAGAGAGAGAGAGACTGGCCAC 480

DB 421 GCAGAGATGAGTGTGCGAGTGTGCTTATGCTTACAGAGAGAGAGAGACTGGCCAC 480

QY 481 TGTGAGGCTTGCAGCGTGTGCGAGTGTGCTTATGCTTACAGAGAGAGAGAGACTGGCCAC 540

DB 481 TGTGAGGCTTGCAGCGTGTGCGAGTGTGCTTATGCTTACAGAGAGAGAGAGACTGGCCAC 540

QY 541 CAGAACACAGTGTGTGAAGAGTGTGCGAGGCGACATCTCAGAGAGCCCAACCATGCTG 600

DB 541 CAGAACACAGTGTGTGAAGAGTGTGCGAGGCGACATCTCAGAGAGCCCAACCATGCTG 600

QY 601 GAGCCGCTGCTTACCTGCGAGCGTGTGCGAGGAGACACTGAGCGGAGTTCAGAGTGCAG 660

DB 601 GAGCCGCTGCTTACCTGCGAGCGTGTGCGAGGAGACACTGAGCGGAGTTCAGAGTGCAG 660

## RESULT 2

US-09-821-831-1

Sequence 1, Application US/09821831

Patent No. US20020137188A1

GENERAL INFORMATION:

APPLICANT: Bartlett, Perry Francis

APPLICANT: Coulson, Elizabeth Jane

APPLICANT: Fielden, Katrina

APPLICANT: Baga, Manuel

APPLICANT: Kilpatrick, Trevor

Db	661	CCCTGGGCTGATGCTGAATGCGAAGAGATCCCTGGTTCATGGAATCCCAAGGTCTACGCC	720
Qy	661	CCCTGGGCTGATGCTGAATGCGAAGAGATCCCTGGTTCATGGAATCCCAAGGTCTACGCC	720
Db	661	CCCTGGGCTGATGCTGAATGCGAAGAGATCCCTGGTTCATGGAATCCCAAGGTCTACGCC	720
Qy	721	CCGAGAGGCTCCGACAGCAACAGCGCCAGACCCAGAGGCTTGAGTCTTCCAGAGCAA	780
Db	721	CCGAGAGGCTCCGACAGCAACAGCGCCAGACCCAGAGGCTTGAGTCTTCCAGAGCAA	780
Qy	781	GACCTTGTAACCCAGTACAGTGGGGGATATGTGACCACTGTGATGGGAGAGTCCCAAGCT	840
Db	781	GACCTTGTAACCCAGTACAGTGGGGGATATGTGACCACTGTGATGGGAGAGTCCCAAGCT	840
Qy	841	GTAGTGACCCGCGGACCAACCGACAAC	867
Db	841	GTAGTGACCCGCGGACCAACCGACAAC	867

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RESULT 3
US-10-388-934-557
Sequence 557, Application US/10388934
Publication No. US20040005547A1
GENERAL INFORMATION:
APPLICANT: Boeers, Franziska
APPLICANT: Suter-Dick, Laura
APPLICANT: Wolf, Detlef
TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
FILE REFERENCE: 21199
CURRENT APPLICATION NUMBER: US/10/388,934
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 0200536.9
PRIOR FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 02015657.6
PRIOR FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 862
SOFTWARE: PatentIn version 3.1
SEQ ID NO 557
LENGTH: 3259
TYPE: DNA
ORGANISM: Rattus norvegicus (No. US20040005547A1way rat)
US-10-388-934-557

Query Match          99.9%; Score 866; DB 15; Length 3259;
Best Local Similarity 100.0%; Pred. No. 9.3e-237;
Matches 866; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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QY 62 GGTCTCCGGAGCGGAGCTGAGCTGAGAGGCGGAGCGGTGACGCGGAGGCGTGAATGAGA 121
Db 61 GGTCTCGGAGCGGAGCTGAGCTGAGAGGCGGAGCGGTGACGCGGAGGCGTGAATGAGA 120

QY 122 GGGCAGGTGCTGCTGCTGCAAGCGGCATGAGACGGCTTCGCGCTGCTGCTGCTGATTCTAG 181
Db 121 GGGCAGGTGCTGCTGCTGCAAGCGGCATGAGACGGCTTCGCGCTGCTGCTGCTGATTCTAG 180

QY 182 GGGTGTCTCTTGAGAGGTGCCAAGAGAGATGTTCCACAGGCTCTTACACCAACGCGAG 241
Db 181 GGGTGTCTCTTGAGAGGTGCCAAGAGAGATGTTCCACAGGCTCTTACACCAACGCGAG 240

QY 242 AGTGTGCAAGGCTCTCAACTTGGGCGAAGGCGTGGCCCAAGCCTTGCGAGAGCAACAGA 301
Db 241 AGTGTGCAAGGCTCTCAACTTGGGCGAAGGCGTGGCCCAAGCCTTGCGAGAGCAACAGA 300

QY 302 CCGTGTGTGAACCTCTGCAATGTTACATTTCCGATGTGTGAGGCGCACTGAGC 361
Db 301 CCGTGTGTGAACCTCTGCAATGTTACATTTCCGATGTGTGAGGCGCACTGAGC 360

QY 362 CGTGCAAGCGGTGACCAAGAGTGCCTGGGCTTGCAGAGATGTCGGCTCCTGTGTGAGAG 421
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Qy	542	AGAACACAGTGTGTGAAGTGTCCACAGAGGGCACATCTCAGACGAAGCCAAACCACTGG	601
Db	541	AGAACACATGTGTGAAGTGTCCAGAGGGCACATCTCAGACGAAGCCAAACCACTGG	600
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Qy	722	CGAGAGGCTCCAGACAGCAGCGCCACAGACCCAGAGACTTGAGGTTCTTCCAGAGCAAG	781
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Qy	782	ACCTTGTACCCAGTACAGTGTGCGGATATGTGTACCACTGTATGTGGCAGCTCCAGGCTTG	841
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Qy	842	TAGTGAACCGCGGACCAACCCGACAAAC	867
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RESULT 4
US-10-101-510-156
; Sequence 156; Application US/10101510
; Publication No. US20030148295A1
GENERAL INFORMATION:
APPLICANT: WAN, JACKSON
APPLICANT: WANG, YIXIN
TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
FILE REFERENCE: 15117.0012
CURRENT APPLICATION NUMBER: US/10/101,510
CURRENT FILING DATE: 2002-03-20
PRIORITY APPLICATION NUMBER: 60/276,947
PRIORITY FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 805
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 156
LENGTH: 3386
TYPE: DNA
ORGANISM: Homo sapiens
US-10-101-510-156

Query Match 72.6%; Score 629.2; DB 14; Length 3386;
Best Local Similarity 85.0%; Pred. No. 2.6e-169;
Matches 716; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

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PUBMED  
 REFERENCE  
 AUTHORS  
 3  
 11042159  
 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,  
 Komori,H., Akiyama,T., Nishii,K., Kitamura,T., Tashiro,H., Itoh,M.,  
 Suni,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A.,  
 Yamamoto,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Kasai,H.,  
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 Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,T.,  
 Okazaki,Y., Muramatsu,M., Inoue,Y., Kikita,A. and Hayashizaki,Y.  
 RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multiplexillary sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)  
 JOURNAL  
 MEDLINE  
 PUBMED  
 REFERENCE  
 AUTHORS  
 4  
 11078861  
 The RIKEN Genome Exploration Research Group Phase II Team and the  
 PANTOM Consortium.  
 Functional annotation of a full-length mouse cDNA collection  
 Nature 409, 685-690 (2001)  
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 AUTHORS  
 5  
 The PANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 6 (bases 1 to 3399)  
 Adachi,Y., Aizawa,K., Akiyama,T., Atakawa,T., Bono,H., Carninci,P.,  
 Fukuda,S., Furuta,M., Hanagaki,T., Hara,A., Hashizume,W.,  
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 Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,X., Sakazume,N.,  
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 Sogabe,Y., Tasami,M., Tagawa,K., Takahashi,F., Takaku-Akahira,S.,  
 Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,  
 Muramatsu,M. and Hayashizaki,Y.  
 Direct Substition  
 Submitted (16-JUL-2001) Yoshihide Hayashizaki. The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute; 1-7-22 Saitoh-cho, Tsurumi-Ku, Yokohama,  
 Kanagawa 220-0045, Japan [E-mail:genome-res@gscc.riken.go.jp,  
 URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,  
 Fax:81-45-503-9216]  
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 CDNA library was prepared and sequenced in Mouse Genome  
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 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
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82	CACCACTCGGTCTGCGGAGCGGACCTGAGCTAGAAAGCTGAGCGCTGCGCGGAGGCGGACGA	141						
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142	ATGAGAGGGGACAGTGTCTGCTGCAAGCGCCATGGAACCGGTGGCTGCTGCTGCTGCTG	201						
169	CTGCTGATCTGAGGAGGTGTCTCTCTGAGAGGTGCGCAAGAGACATGTTCCAGAGCGCTGTAC	228						
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262	ACCCACAGTGGAGAGTGTCTGCAAAAGCTGCACTTGGCGGAGAGGTGGCCAGCTTTC	321						
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622	GCCAAACAGTGAAGCCCGTGTCTACCCCTGCAAGCGTGTGCGAGGACACTGAGCGCCAGTTA	681						
649	CAGGAGTGAAGCCCGTGTGTGATGCTGATATGCGAAGAGATCCCTGGTGAATGGATCCCA	708						
682	CAGGAGTGAAGCCCGTGTGTGATGCTGATATGCGAAGAGATCCCTGGTGAATGGATCCCA	741						
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769	CTTCCAGAGCAAGACTTGTATCCCATGATACAGTGCAGATATGTGACACTGTGTGATGGCG	828						
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829	AGCTCCAGACTGTATGTGACCGCGGCGACCAACGACAC	867						

Db 862 AGCTCCAGCCTGATGACCCGAGGCGACCCGCTGACAC 900

RESULT 2  
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DEFINITION U1-M-HD0-ckg-e-06-0-U1.r1 NIH\_BMAP\_HD0 Mus musculus cDNA clone  
IMAGE:30608261.5', mRNA sequence.  
CF736981  
ACCESSION CF736981  
VERSION CF736981.1 GI:37633317  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.  
TITLE NIH-MGC <http://mgi.nci.nih.gov/>.  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: Dr. James Lin University of Iowa  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/mouse1.html>  
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(BMAP)  
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Site 2: Not I. The library was constructed according  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured RNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with oligo-dT  
primer containing a Not I site. Double strand cDNA was  
size selected according to mRNA size fraction, ligated  
with EcoR I adaptor, digested with NotI and then cloned  
directionally into PYX\_Asc vector. The library tag  
is TTTATGAGT. This library was created for the University  
Iowa Brain Anatomy Project (BMAP). Gene Discovery in the  
Developing Mouse Nervous System", supported by National  
Institute of Mental Health (NIMH)."

ORIGIN  
Query Match 69.5% Score 602.6; DB 14; Length 714;  
Best Local Similarity 93.3% Pred. No. 3.1e-124;  
Matches 656; Conservative 0; Mismatches 34; Indels 13; Gaps 2;

QY 2 CAGCTCCGCGCGGCGAGCGCTGAGCGCATGCGACTCA-----GCGCAG 54  
DB 12 CAGCTCCGCGCGGCGGCGCTGAGCGCGCAGCGCATGCGACTCAGCGCCGAG 71  
QY 55 CACCATCGCTCGCGAGCGGAGCTGAGTAAGGCGGCGCTGACCGCGGAGGCGTGA 114  
DB 72 CACCATCGCTCGCGAGCGGAGCTGAGTAAGGCGCTGCGCGGAGGCGAGCA 131  
QY 115 ATGAGAGGAGGAGTGTGCTGCTGCGAGCGCCATGACCGGCTGCGC-----CTGCTGCTG 168

Db 112 ATGAGAGGAGGAGTGTGCTGCTGAGCGCGCATGAGACCGGCTGCGCTGCTGCTG 191

QY 169 CTGCTGATCTTAAGGGGGTCTCTGAGAGTGGCAGAGGAGCATGTTCACAGGCTGTAC 228  
DB 192 CTGCTGCTTCTAGGGGTTCTCTTGGAGTGGCAGAGGAGCATGTTCACAGGCTGTAC 251

QY 229 ACCCAGCGGAGAGTGTGCAAGAGCTGTGCAACTTGTGGGAGGAGGCGTGGCCAGGCTTGC 288  
DB 252 ACCCAGCGGAGAGTGTGCAAGAGCTGTGCAACTTGTGGGAGGAGGCGTGGCCAGGCTTGC 311

QY 289 GGAGCCACCAACGATGCTGTGAACCTGCGCTGGAACAATGTACATCTCCGATGTGGG 348  
DB 312 GGAGCCACCAACGATGCTGTGAACCTGCGCTGGAACAATGTACATCTCCGATGTGGG 371

QY 349 AGCGCCACTGAGCCGCTGCAAGCCGTGCAACCGAGTCCCTGCGCTGCAAGCATGTCCGCT 408  
DB 372 AGCGCCACTGAGCCGCTGCAAGCCGTGCAACCGAGTCCCTGCGCTGCAAGCATGTCCGCT 431

QY 409 CCTGTGTGAGGAGCAGACGATGATGTGCAATGTGCTTACTTACCAAGACGAG 468  
DB 432 CCTGTGTGAGGAGCAGACGATGATGTGCAATGTGCTTACTTACCAAGACGAG 491

QY 469 GAGACTGGCCACTGTGAGGCTTGCAGAGCTGTGCGAGTGGGCTCGGACTCGTGTCTCC 528  
DB 492 GAGACTGGCCACTGTGAGGCTTGCAGAGCTGTGCGAGTGGGCTCGGACTCGTGTCTCC 551

QY 529 TGCAGAGCAAAACAGAACACAGTGTGTGAAGATGCCAGAGGCACTATCAACGAA 588  
DB 552 TGCAGAGCAAAACAGAACACAGTGTGTGAAGATGCCAGAGGCACTATCAACGAA 611

QY 589 GCCAACACAGTGAACCCGCTGCTGACCGCTGCAAGTGTGCGAGACATGAGCGCAGTA 648  
DB 612 GCCAACACAGTGAACCCGCTGCTGACCGCTGCAAGTGTGCGAGACATGAGCGCAGTA 671

QY 649 CCGAGTGCACGCGCTGCGCTGATGTGAATGCGAAGATCC 691  
DB 672 CGGAGTGCACGCGCTGCGCTGATGTGAATGCGAAGATCC 714

RESULT 3  
LOCUS B1735945 690 bp mRNA linear EST 20-SEP-2001  
DEFINITION B1735945 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:5367638.5',  
mRNA sequence.  
B1735945  
ACCESSION B1735945  
VERSION B1735945.1 GI:15712958  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.  
TITLE NIH-MGC <http://mgi.nci.nih.gov/>.  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: The Cepko Laboratory  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: InCyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLNL1935 row: 1 column: 15  
High quality sequence stop: 687.  
Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
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FEATURES  
source







contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGGAGAGGAAGAATCCAAAGACGGCTTTTTTTTTTTTNN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGGAGAGGATTCGCCGTATTATAAATATATCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified plasmidscript KS(+) after bulk excision from Lambda

FLC I.

## ORIGIN

Query Match	59.0%	Score 511.8	DB 10	Length 645
Best Local Similarity	91.9%	Pred. No. 6.1e-104		
Matches 567	Conservative	0	Mismatches 37	Indels 13
				Gaps 2

OY	2	CAGCTCCGCGGGGCAAGACCGGCTGAGAGCGCATCCAGTTCAAGTCA-----GGCAG	54
Db	22	CAGCTTCGGCGGGCAGCGGGCGCTGAGAGCGCAGCGCAAGCTTCAGTCAAGCGCGAG	81
OY	55	CACCATCGTCTGCGGAGCGGACTGAGTAAAGCGGAAGCGCTGACGCCGAGGCGTGTCA	114
Db	82	CACCTACGGTCCGCGAGAGCGGACTAGCTAGTAAGCTGAGCGCTGTCTCGCCGAGGAGCA	141
OY	115	ATGAGAGAGGGCAGGAGTCTGCTGCAGCGCGCATAGACCGGCTCGCG-----CTGCTGCTG	168
Db	142	ATGAGAGAGGGCAGGAGTCTGCTGCTGCAGCGCGCATAGACCGGCTGCGCTGTGTTGCTGTG	201
OY	169	CTGCTGATTCTAAGGAGTCTCTGTGAGAGTGCACAGAGACATGTTTCCACAGGCTCTTAC	228
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OY	229	ACCACAGCGGAGAGTGTGCTGCAGGAGCTTGCCTTGCAGGAGGCGTGGCCAGGCTTGC	288
Db	262	ACCACAGTGGAGAGTGTGCTGCAGGAGCTTGCCTTGCAGGAGGAGTGTGGCCAGGCTTGC	321
OY	289	GAGGCGAACACAGACCGTGTGTAAACCTCGCCCTGGACAAATGTAAKATTCCTCCGATGTGAG	348
Db	322	GGAGCGAACACAGACCGTGTGTAAACCTCGCCCTGGAGAGTGTAAAGTTACGTTCTCTACGTTGAT	381
OY	349	AGCGGCACCTGAGCCGTGCAGGCGGTGCACCGAGTGTCTTGAGGCTTGACAGACATGTCGCT	408
Db	382	AGCGGCACCGGACCGGTGCAGGCGGTGCACCGAGTGTCTTGAGGCTTGACAGACATGTCGCT	441
OY	409	CCCTGTGTGAGGAGCAGATGCATGATGCATGTGCTTATGTGGCTACTACAGAGACGAG	468
Db	442	CCCTGTGTGAGGAGCAGATGCATGATGCATGTGCTTATGTGGCTACTACAGAGACGAG	501
OY	469	GAGACTGGCCACTGTGAGGCTTGCAGCGTGTGCGAGGTGGGCTCGGAGCTCGTGTCTCC	528
Db	502	GAGACTGGCCGCTGCGAGGCTTGCAGCGTGTGCGAGGTGGGCTCGGAGCTCGTGTCTCC	561
OY	529	TGCGCAGACAAACAGAACACAGTGTGTGAAGATGCCACAGAGGACATATCTCAGACGAA	588
Db	562	TGCGCAGACAAACAGAACACAGTGTGTGAAGATGCCACAGAGGACATATCTCAGATGA	621
OY	589	GCCAAACAGTGCAGCC	605
Db	622	ACCAACCAAGTTGGACC	638

RESULT 7	
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LOCUS	622 bp mRNA linear EST 26-OCT-200
DEFINITION	BB655751 RIKEN full-length enriched, 12 days embryo spinal ganglion
ACCESSION	Mus musculus cDNA clone D130022N18.5', mRNA sequence.
VERSION	BB655751
KEYWORDS	BB655751.1 GI:16489579
SOURCE	EST.
ORGANISM	Mus musculus (house mouse)
	Mus musculus

REFERENCE  
AUTHORS

TITLE  
JOURNAL  
COMMENT

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanaizaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Komono, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Satto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takekida, Y., Tanaka, T., Toyota, T., Muramatsu, M. and Hayashizaki, Y. (1999) The Riken Mouse ESTs (Arakawa, T., et al. 2001)

**FEATURES**  
**SOURCE**

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/lab_host="DH10B"
/clone_id="R1KEN full-length enriched, 12 days embryo
spinal ganglion"
/notes="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAAGAGAGAGCGCCGACACGAGTTTCTTTTCTTTN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adaptor of sequence [5',
GAAGAGAGAGTTCTCGATTATTAATTAATATCCCCCCCCCC 3']. cDNA
was cleaved with BamHI and XhoI. Vector: a modified
pBlueScript KS(+) after bulk excision from Lambda FLX I."

```

ORIGIN



Db 601 CAGAGCCCAAGCTCCGAGTGCACAGCTGGGCCAAGCCCAAGTGCAGAGATCCCTGG 660

QY 696 TCGATGATCCCAAGGTCTACGCCCCGAGAG 728

Db 661 CCGTGTATTAACCCCGGTCAACCCCAAGAG 693

RESULT 9  
CB725789 490 bp mRNA linear EST 11-APR-2003  
LOCUS CB725789  
DEFINITION AMGNNUC:NRHY7-00043-A7-A nrhy7 (10850) Rattus norvegicus cDNA clone  
ACCESSION CB725789  
VERSION CB725789.1 GI:29792714  
KEYWORDS EST.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 490)  
REFERENCE 1 (bases 1 to 490)  
AUTHORS Amgen EST Program.  
TITLE Amgen Rat EST Program  
JOURNAL Unpublished (2003)  
COMMENT Contact: Dan Fitzpatrick  
Amgen, Inc  
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA  
Tel: 805 447-4881  
Plate: 00043 row: a column: 7.

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ORIGIN

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Best Local Similarity 99.4%; Pred. No. 2,9e-96;  
Matches 479; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 9 CAGCTCCGGGGCAGAGGCGCTGAGCGCATGCAATTCACTCAGCGCAGCAACCATC 68

QY 62 GGTCTGGAGAGGAGCTGAGCTAGAAAGCGAGCGCTGACGCGGAGAGCGTGCATGAGA 121

Db 69 GGTCTGGAGAGGAGCTGAGCTAGAAAGCGAGCGCTGACGCGGAGAGCGTGCATGAGA 128

QY 122 GGGCAGGTGCTGCTGCTGAGCGCATGAGACCGGCTGCTGCTGCTGCTGCTGCTGCTG 181

Db 129 GGGCAGGTGCTGCTGCTGAGCGCATGAGACCGGCTGCTGCTGCTGCTGCTGCTGCTG 188

QY 182 GGGAGTCTCTGAGAGGTGCGCAAGAGACATGTTCCACAGGCGCTGACACCAAGCGAG 241

Db 189 GGAATGCTCTTGAAGGTGCGCAAGAGACATGTTCCACAGGCGCTGACACCAAGCGAG 248

QY 242 AGTCTGCAAAAGCTGCAACTTGGCGAAGCGTGGCCCAAGCCCTGCGAGCCCAACAGA 301

Db 249 AGTCTGCAAAAGCTGCAACTTGGCGAAGCGTGGCCCAAGCCCTGCGAGCCCAACAGA 308

QY 302 CCGGTGTGAACCTGCTGAGACATGTTACATTTCCGATGCGAGGCGCACTGAGC 361

Db 309 CCGGTGTGAACCTGCTGAGACATGTTACATTTCCGATGCGAGGCGCACTGAGC 368

QY 362 CGTGAAGCGGTGACCGAGTGCCTGGCGCTGACAGACATGTCGCTCCCTGTGTGAGG 421

Db 369 CGTGAAGCGGTGACCGAGTGCCTGGCGCTGACAGACATGTCGCTCCCTGTGTGAGG 428

QY 422 CAGACATGAGATGTGAGATGCGCTATGCGCTACTACCAAGAGAGAGACTGGCCACT 481

Db 429 CAGACATGAGATGTGAGATGCGCTATGCGCTACTACCAAGAGAGAGACTGGCCACT 488

QY 482 GT 483

Db 489 GT 490

RESULT 10  
CB716157 517 bp mRNA linear EST 10-APR-2003  
LOCUS CB716157  
DEFINITION AMGNNUC:NRHY5-00132-C2-A W Rat hypothalmus (10471) Rattus  
norvegicus cDNA clone nrhy5-00132-c2 5', mRNA sequence.  
ACCESSION CB716157  
VERSION CB716157.1 GI:29773305  
KEYWORDS EST.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 517)  
REFERENCE 1 (bases 1 to 517)  
AUTHORS Amgen EST Program.  
TITLE Amgen Rat EST Program  
JOURNAL Unpublished (2003)  
COMMENT Contact: Dan Fitzpatrick  
Amgen, Inc  
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA  
Tel: 805 447-4881  
Plate: 00132 row: c column: 2.

FEATURES  
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kb fraction 6 and 7"

ORIGIN

Query Match 55.0%; Score 477.2; DB 14; Length 517;  
Best Local Similarity 97.4%; Pred. No. 3e-96;  
Matches 485; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2 CAGCTCCGGGGCAGAGGCGCTGAGCGCATGCAATTCACTCAGCGCAGCAACCATC 61

Db 20 CAGCTCCGGGGCAGAGGCGCTGAGCGCATGCAATTCACTCAGCGCAGCAACCATC 79

QY 62 GGTCTGGAGAGGAGCTGAGCTAGAAAGCGAGCGCTGACGCGGAGAGCGTGCATGAGA 121

Db 80 GGTCTGGAGAGGAGCTGAGCTAGAAAGCGAGCGCTGACGCGGAGAGCGTGCATGAGA 129

QY 122 GGGCAGGTGCTGCTGCTGAGCGCATGAGACCGGCTGCTGCTGCTGCTGCTGCTGCTG 181

Db 140 GGGCAGGTGCTGCTGCTGAGCGCATGAGACCGGCTGCTGCTGCTGCTGCTGCTGCTG 189

QY 182 GGGAGTCTCTGAGAGGTGCGCAAGAGACATGTTCCACAGGCGCTGACACCAAGCGAG 241

Db 200 GGAATGCTCTTGAAGGTGCGCAAGAGACATGTTCCACAGGCGCTGACACCAAGCGAG 259

QY 242 AGTCTGCAAAAGCTGCAACTTGGCGAAGCGTGGCCCAAGCCCTGCGAGCCCAACAGA 301

Db 260 AGTCTGCAAAAGCTGCAACTTGGCGAAGCGTGGCCCAAGCCCTGCGAGCCCAACAGA 319

QY 302 CCGGTGTGAACCTGCTGAGACATGTTACATTTCCGATGCGAGGCGCACTGAGC 361

Db 320 CCGGTGTGAACCTGCTGAGACATGTTACATTTCCGATGCGAGGCGCACTGAGC 379

QY 362 CGTGAAGCGGTGACCGAGTGCCTGGCGCTGACAGACATGTCGCTCCCTGTGTGAGG 421

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using bw model

Run on: March 12, 2004, 16:27:17 ; Search time 60 Seconds  
(without alignments)

1181.990 Million cell updates/sec

Title: US-09-821-831-4

Sequence: 1 MRRAGAACSMRRLRLILL.....MTTWGSSQPVVTRGTTN 251

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1387	100.0	251	AAV92372	p75-NTR (
2	1387	100.0	425	AAV92370	p75-NTR (
3	1387	100.0	425	AAE21671	Rat neuro
4	1387	100.0	425	ADB81367	Rat nerve
5	1387	100.0	425	ADB63294	Rat Prote
6	1244	89.7	427	AAV33483	Human neu
7	1244	89.7	427	AAV33483	Human NGF
8	1244	89.7	427	AAV33483	Human NGF
9	1244	89.7	427	AAE21670	Human neu
10	1244	89.7	427	ABP98489	Human act
11	1244	89.7	427	ADB81366	Human ner
12	1244	89.7	427	ADB63296	Human ner
13	1244	89.7	427	ADB63296	Human ner
14	1244	89.7	427	ABP71146	Human NGF
15	1216	87.7	427	ABP71146	Human p75
16	1133	81.7	427	ABP71146	Human p75
17	866	62.4	159	ADA49702	Extracell
18	402	29.0	76	AAW94643	TNF-R ext
19	402	29.0	76	AAW94643	Human TNF
20	329	23.7	58	AAW40521	Rat p75
21	307	22.1	58	AAW40520	Human p75
22	270	19.5	58	AAW40522	Chicken p
23	216.5	15.6	277	AAW76996	Deduced 8
24	215.5	15.5	461	AAW57927	Rat Prote
25	214	15.4	277	AAW74737	ACT-4 cel

26	214	15.4	277	2	AAW79904	AAW79904
27	214	15.4	277	4	AAW35329	ACT-4-h-1
28	214	15.4	277	6	AAW50522	Human OX4
29	214	15.4	277	4	AAW16569	Human tum
30	214	15.4	277	6	ABP71700	Human met
31	214	15.4	277	6	ABP71700	Human OX4
32	214	15.4	277	6	ABP71700	Human OX4
33	211	15.2	204	5	ABW81467	Binding d
34	208	15.0	197	3	AAW79205	Murine TA
35	208	15.0	197	6	AAW79205	Soluble h
36	207	14.9	144	6	ABJ37098	Human sol
37	205.5	14.8	909	2	AAW64485	Concane
38	204.5	14.7	336	2	AAW33360	Human Fas
39	203.5	14.7	277	6	AAW79207	TBP(20-19
40	203.5	14.7	277	6	ABU60694	Membrane
41	203.5	14.7	283	2	AAW05809	Human mem
42	203.5	14.7	283	2	AAW60045	Human tum
43	203.5	14.7	283	2	AAW69238	Human TNF
44	203.5	14.7	283	2	AAW87591	Herpesvir
45	203.5	14.7	283	2	AAW06468	Human tum

## ALIGNMENTS

RESULT 1  
ID AAV92372 standard; protein, 251 AA.

AC	AAV92372;	
XX		
DT	10-AUG-2000 (first entry)	
XX		
DE	p75-NTR (neurotrophin receptor) extracellular portion.	
XX		
KM	p75 neurotrophin receptor; extracellular; p75-NTR; death receptor;	
KM	apoptosis; death signal domain; antagonist; cell survival; cytotoxic;	
KM	neurotrophic; anticonvulsant; antiparkinsonian; antidiabetic; anti-HIV; virucide;	
XX		
OS	Rattus sp.	
XX		
PN	WO200020578-A1.	
XX		
PD	13-APR-2000.	
XX		
PF	05-OCT-1999; 99WC-AU000860.	
XX		
XX	06-OCT-1998; 98AU-00006353.	
PR	07-OCT-1998; 98AU-00006351.	
XX	01-JUN-1999; 99AU-00000701.	
PA	(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.	
XX		
PI	Bartlett PF, Coulson EJ, Fielden K, Baca M, Kilpatrick T;	
XX	Surinder C;	
XX		
DR	WPI; 2000-328933/28.	
XX	N-PSDB; AAA09358.	
PT	Novel nucleic acids encoding a peptide capable of facilitating the death	
PT	of a cell, useful for antagonizing cell death signal function and	
PT	promoting cell death, e.g. for treating cancer.	
XX		
PS	Disclosure; Page 72-73; 80pp; English.	
XX		
CC	This sequence is the extracellular portion (or ligand binding molecule)	
CC	of rat p75 neurotrophin receptor (p75-NTR). p75-NTR is multifunctional	
CC	and is capable of acting as a death receptor. Elevated p75-NTR expression	
CC	results in increased death in vitro and in vivo. It has been determined	
CC	that the death signal is not the cytoplasmic motif known as the death	
CC	domain, but is a region adjacent to the membrane domain on p75-NTR.	
CC	Identification of this region provides an opportunity to modulate cell	

CC survival by antagonizing the death signalling region or promoting  
 CC apoptosis by providing cells with the genetic material to express the  
 CC death signalling region adjacent, proximal, or otherwise juxtaposed or  
 CC associated membrane of a cell or to express the death signalling region  
 CC in multimeric form. The polypeptides and methods of the invention are  
 CC useful for inhibiting, reducing or antagonizing p75-NTR-mediated death  
 CC signals in neural cells. In particular, the methods are used for the  
 CC treatment or prophylaxis of disease conditions associated with neural  
 CC death or where cell death is to be promoted such as in treating or  
 CC preventing cancer growth and/or development. Other diseases capable of  
 CC treatment include neurodegenerative diseases, such as cerebral palsy,  
 CC trauma induced paralysis, vascular ischemia associated with stroke,  
 CC neural tumors, motorneuron diseases, Parkinson's disease, Huntington's  
 CC disease, Alzheimer's disease, multiple sclerosis and peripheral  
 CC neuropathies associated with diabetes, heavy metal or alcohol toxicity,  
 CC renal failure, and/or infectious diseases such as Herpes, rubella,  
 CC measles, chicken pox, HIV and HTLV-1 (all claimed). The methods are also  
 CC useful for treating neurons or glia damaged by trauma or disease  
 CC (claimed). Animals which can be treated include humans, livestock  
 CC animals, laboratory test animals, companion animals, and captive wild  
 CC animals

XX Sequence 251 AA;

Query Match 100.0%; Score 1387; DB 3; Length 251;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-99;  
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 MRRAGAACSAMDRRLRLILLIIGVSSGAKETCTGLYTHSGECKKCNIGBGVAQPCGA 60  
 QY 61 NQTVCEPCLDNVTFSDVVSATPECKPCTBCLGLQSNAPCVADAVCAAGYQDEET 120  
 Db 61 NQTVCEPCLDNVTFSDVVSATPECKPCTBCLGLQSNAPCVADAVCAAGYQDEET 120  
 QY 121 GHCEACSVCEVSGGLVFSGCCDKONTVCEBCEPBGTYDEANHVDPCLPCTVCEDETEROLRE 180  
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 QY 241 QPVVTRGTTDN 251  
 Db 241 QPVVTRGTTDN 251

RESULT 2  
 ID AAY92370 standard; protein; 425 AA.  
 XX AAY92370;

XX 10-AUG-2000 (first entry)  
 DE p75-NTR (neurotrophin receptor).  
 XX

XX p75 neurotrophin receptor; p75-NTR; death receptor; apoptosis;  
 KM death signal domain; antagonist; cell survival; cytosolic;  
 KM neuroprotective; antiparkinsonian; antidiabetic; anti-HIV; virocidic;  
 KM neurotrophic; anticonvulsant; cerebroprotective.  
 XX

OS Homo sapiens.  
 XX  
 PN WO2000020578-A1.  
 XX  
 PD 13-APR-2000.  
 XX  
 PF 05-OCT-1999; 99WC-AUD000860.  
 XX  
 PR 06-OCT-1998; 98AU-00006353.

PR 07-OCT-1998; 98AU-00006351.  
 PR 01-JUN-1999; 99AU-00000701.  
 XX  
 XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
 XX  
 XX Battist PF, Coulson EJ, Fieldew K, Baca M, Kilpatrick T,  
 PI Sundarar C;  
 XX WPI; 2000-328933/28.  
 DR N-PSDB; AAA09356.  
 DR  
 XX  
 XX Novel nucleic acids encoding a peptide capable of facilitating the death  
 PT of a cell, useful for antagonizing cell death signal function and  
 PT promoting cell death, e.g. for treating cancer.  
 PS Disclosure; Page 69-70; 80pp; English.

CC This is the human p75 neurotrophin receptor (p75-NTR). p75-NTR is  
 CC multifunctional and is capable of acting as a death receptor. Elevated  
 CC p75-NTR expression results in increased death in vitro and in vivo. It  
 CC has been determined that the death signal is not the cytoplasmic motif  
 CC known as the death domain, but is a region adjacent the membrane domain  
 CC on p75-NTR. Identification of this region provides an opportunity to  
 CC modulate cell survival by antagonizing the death signalling region or  
 CC promoting apoptosis by providing cells with the genetic material to  
 CC express the death signalling region adjacent, proximal, or otherwise  
 CC juxtaposed or associated membrane of a cell or to express the death  
 CC signalling region in multimeric form. The polypeptides and methods of the  
 CC invention are useful for inhibiting, reducing or antagonizing p75-NTR-  
 CC mediated death signals in neural cells. In particular, the methods are  
 CC used for the treatment or prophylaxis of disease conditions associated  
 CC with neural death or where cell death is to be promoted such as in  
 CC treating or preventing cancer growth and/or development. Other diseases  
 CC capable of treatment include neurodegenerative diseases, such as cerebral  
 CC palsy, trauma induced paralysis, vascular ischemia associated with  
 CC stroke, neural tumors, motorneuron diseases, Parkinson's disease,  
 CC Huntington's disease, Alzheimer's disease, multiple sclerosis and  
 CC peripheral neuropathies associated with diabetes, heavy metal or alcohol  
 CC toxicity, renal failure, and/or infectious diseases such as Herpes,  
 CC rubella, measles, chicken pox, HIV and HTLV-1 (all claimed). The methods  
 CC are also useful for treating neurons or glia damaged by trauma or disease  
 CC (claimed). Animals which can be treated include humans, livestock  
 CC animals, laboratory test animals, companion animals, and captive wild  
 CC animals

XX Sequence 425 AA;

Query Match 100.0%; Score 1387; DB 3; Length 425;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-99;  
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRAGAACSAMDRRLRLILLIIGVSSGAKETCTGLYTHSGECKKCNIGBGVAQPCGA 60  
 Db 1 MRRAGAACSAMDRRLRLILLIIGVSSGAKETCTGLYTHSGECKKCNIGBGVAQPCGA 60  
 QY 61 NQTVCEPCLDNVTFSDVVSATPECKPCTBCLGLQSNAPCVADAVCAAGYQDEET 120  
 Db 61 NQTVCEPCLDNVTFSDVVSATPECKPCTBCLGLQSNAPCVADAVCAAGYQDEET 120  
 QY 121 GHCEACSVCEVSGGLVFSGCCDKONTVCEBCEPBGTYDEANHVDPCLPCTVCEDETEROLRE 180  
 Db 121 GHCEACSVCEVSGGLVFSGCCDKONTVCEBCEPBGTYDEANHVDPCLPCTVCEDETEROLRE 180  
 QY 121 GHCEACSVCEVSGGLVFSGCCDKONTVCEBCEPBGTYDEANHVDPCLPCTVCEDETEROLRE 180  
 Db 121 GHCEACSVCEVSGGLVFSGCCDKONTVCEBCEPBGTYDEANHVDPCLPCTVCEDETEROLRE 180  
 QY 181 CTPWADACEEIPGRWIPRSTPEGSDSTAPSTQEPPEVPPEODLVPSVTADMTTWGSS 240  
 Db 181 CTPWADACEEIPGRWIPRSTPEGSDSTAPSTQEPPEVPPEODLVPSVTADMTTWGSS 240  
 QY 241 QPVVTRGTTDN 251  
 Db 241 QPVVTRGTTDN 251

RESULT 3

AAE21671.  
ID AAE21671 standard; protein; 425 AA.  
XX  
AC AAE21671;  
XX  
DT 16-JUL-2002 (first entry)  
XX  
DE Rat neurotrophic receptor (p75NTR) protein.  
XX  
KW Rat; diabetic neuropathy; therapy; neurotrophic receptor; p75NTR;  
KW drug screening; receptor.  
XX  
OS Rattus sp.  
XX  
FN W0200218955-A1.  
PN  
PD 07-MAR-2002.  
XX  
PF 29-AUG-2001; 2001MC-GB003859.  
XX  
FR 01-SEP-2000; 2000GB-00021609.  
XX  
PA (UTMA-) UNIV VICTORIA MANCHESTER.  
XX  
PI Tomlinson DR;  
XX  
DR WPI; 2002-329796/36.  
XX  
PT Detecting neuropathy, evaluating effect/efficacy of a drug for treating  
PT neuropathy or screening compounds to assess their side effects causing  
PT neuropathy, by detecting 75 kDa Neurotrophic Receptor in patient sample.  
PS  
PS Disclosure; Fig 2; 33pp; English.  
XX  
XX The invention relates to an in vitro test for neuropathy, for evaluating  
CC whether a subject will benefit from a putative drug for treating  
CC neuropathy. The method comprising detecting for the presence of a 75 kDa  
CC neurotrophic receptor (p75NTR) in a body fluid sample. The invention is  
CC used for diagnosing neuropathy, particularly diabetic neuropathy, for  
CC evaluating whether or not a subject will benefit from a putative drug for  
CC treating neuropathy, for screening a compound to assess whether or not a  
CC compound causes neuropathy, monitoring the health status of a subject  
CC with or at risk of developing neuropathy and testing whether or not a  
CC subject is complying with therapeutic regime for treating diabetes. The  
CC method is also useful for making a detailed analysis such as a clinical  
CC trial of a drug targetted at diabetic neuropathy. The present sequence is  
CC rat p75NTR protein  
SQ  
Sequence 425 AA;  
Query March 100.0%; Score 1387; DB 5; Length 425;  
Best Local Similarity 100.0%; Pred. No 2,1e-99;  
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0  
1 MRPAGAAACSMADRLRLILLILLIGVSSGGAKETCSGLVTHSGECCKACNLGEGVAPCGA 60  
1 MRPAGAACSMADRLRLILLILLIGVSSGGAKETCSGLVTHSGECCKACNLGEGVAPCGA 60  
61 NQTVCEPCDLNMTFSSVVSATBPCPCPCGGLGQNSAPCEADADAYCRCAVGYODEET 120  
61 NQTVCEPCDLNMTFSSVVSATBPCPCPCGGLGQNSAPCEADADAYCRCAVGYODEET 120  
121 GHCEAGCVCVGGGLVFSQCDKQNTVCEBCEPGTYSDEANHVDPCLPCTVCEPTEROLR 180  
121 GHCEAGCVCVGGGLVFSQCDKQNTVCEBCEPGTYSDEANHVDPCLPCTVCEPTEROLR 180  
121 GHCEAGCVCVGGGLVFSQCDKQNTVCEBCEPGTYSDEANHVDPCLPCTVCEPTEROLR 180  
121 GHCEAGCVCVGGGLVFSQCDKQNTVCEBCEPGTYSDEANHVDPCLPCTVCEPTEROLR 180  
181 CTTPADDECEIIGRWIPSTPEGSDSTAPSTOPEVPPRODVLVPSIVADMTTWWGSS 240  
181 CTTPADDECEIIGRWIPSTPEGSDSTAPSTOPEVPPRODVLVPSIVADMTTWWGSS 240  
241 QPVVTRGTTDN 251

Db 241 QPVTGRTDN 251

RESULT 4  
ADBB1367  
ID ADBB1367 standard; protein; 425 AA.  
XX ADBB1367;  
XX  
XX  
DT 04-DEC-2003 (first entry)  
XX  
XX  
DE Rat nerve growth factor receptor p75 protein.  
XX  
XX  
KW rat; CARD-3; CARD-4; caspase recruitment domain; apoptosis; p75;  
KW tumour necrosis factor; TNF; neutrophin receptor; cancer;  
KW autoimmune disorder; systemic lupus; immune mediated glomerulonephritis;  
KW viral infection; neurologically; retinitis pigmentosa; haematologic;  
KW chronic neutropenia; myocardial infarction; stroke; RIP; RICK; CARDIAX.  
XX  
XX  
XX Rattus sp.  
XX  
XX US2002061833-A1.  
XX  
XX 23-MAY-2002.  
XX  
XX 26-DEC-2000; 2000US-00748537.  
XX  
XX 06-FEB-1998; 98US-00019942.  
XX 17-JUN-1998; 98US-00099041.  
XX  
XX (BEST/) BERTIN J.  
XX (CHAO/) CHAO M V.  
XX  
XX Bertin J, Chao MV;  
XX  
XX WPI, 2003-657125/62.  
XX  
XX Detecting compounds which alter binding of the caspase recruitment domain  
XX (CARD) of CARD-3 polypeptide to the neutrophin receptor p75 is useful  
XX to provide compounds for treating CARD-3 mediated disorders.  
XX  
XX  
XX Disclousure; Fig 14; 40pp; English.  
XX  
XX  
XX This invention relates to two novel genes CARD-3 and CARD-4 (caspase  
XX recruitment domains) which are mediators of apoptosis and are useful in  
XX the identification of compounds that modulate apoptosis. Specifically  
XX CARD-3 (also known as RIP2, RICK and CARDIAX) is known to be a mediator  
XX of p75 (a member of the tumour necrosis factor (TNF) family), and is  
XX believed to provide the switch for cell survival and cell death decisions  
XX mediated by this p75 neutrophin receptor. Accordingly these genes, and  
XX the proteins encoded thereof, are linked to certain disorders associated  
XX with an increased number of cells surviving and proliferating when  
XX apoptosis is inhibited. These include cancer, autoimmune disorders e.g.  
XX systemic lupus and immune mediated glomerulonephritis, viral infections  
XX such as those caused by the herpesvirus, neurological disorders such as  
XX retinitis pigmentosa, haematologic diseases including chronic  
XX neutropenia, as well as myocardial infarction and strokes. The present  
XX invention further describes a novel method for determining whether a test  
XX compound alters the binding of CARD-3 to p75, which comprises measuring  
XX the binding of a polypeptide containing the CARD domain of CARD-3 to a  
XX polypeptide comprising the death domain of p75 in the presence and  
XX absence of the test compound, and determining if binding is altered. This  
XX polypeptide is the rat nerve growth factor receptor protein sequence of  
XX the invention.  
XX  
XX  
XX Sequence 425 AA;  
XX  
XX  
XX Query Match 100.0%; Score 1387; DB 7; Length 425;  
XX Best Local Similarity 100.0%; Pred. No. 2.1e-99;  
XX Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 1 MRRAGAACSNDRRLILLILGVSGGAKRTCTGLYTHSGECCXCNLDGVAQPPGCA 60

Db 1 MRRAGAACSMRRLRLLLLLIGVSSGAKETCTGLYTHSGECCKACNLGSGVAPCGA 60  
 QY 61 NOTVCEPCLDNVTFSDVVSATPECKPCTECLGLQMSAPCVADAVCRCAVGYODEET 120  
 Db 61 NOTVCEPCLDNVTFSDVVSATPECKPCTECLGLQMSAPCVADAVCRCAVGYODEET 120  
 QY 121 GHCEACSVCEVSGVLSGFCODKQNTVCEBCEPGTYSDEANHVDPCLPCTVCEDETEROLRE 180  
 Db 121 GHCEACSVCEVSGVLSGFCODKQNTVCEBCEPGTYSDEANHVDPCLPCTVCEDETEROLRE 180  
 QY 181 CTPWADACEEIPGRWIPRSTPEGSDSTAPSTOEPEVPEODLVPSIVADVTTWGS 240  
 Db 181 CTPWADACEEIPGRWIPRSTPEGSDSTAPSTOEPEVPEODLVPSIVADVTTWGS 240  
 QY 241 QPVYTRGTTDN 251  
 Db 241 QPVYTRGTTDN 251

## RESULT 5

ID ADE63294 standard; protein; 425 AA.  
 ADE63294

AC ADE63294;  
 XX

DT 29-JAN-2004 (first entry)  
 XX

DE Rat Protein P07174, SEQ ID NO 9231.  
 XX

KM Rat, pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
 XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
 XX

OS Rattus norvegicus.  
 XX

PN MO2003016475-A2.  
 XX

PD 27-FEB-2003.  
 XX

PF 14-AUG-2002; 2002WO-US025765.  
 XX

PR 14-AUG-2001; 2001US-0312147P.  
 XX

PR 01-NOV-2001; 2001US-0346382P.  
 XX

PR 26-NOV-2001; 2001US-0333347P.  
 XX

PA (GEHO) GEN HOSPITAL CORP.  
 XX

PA (FARB) BAYER AG.  
 XX

PI Woolf C, D'urso D, Befort K, Costigan M;  
 XX

DR WPI; 2003-268312/26.  
 XX

DR GENBANK; P07174.  
 XX

PT New composition comprising two or more isolated polypeptides, useful for  
 XX preparing a medicament for treating pain in an animal.  
 XX

PS Claim 1; Page; 1017pp; English.  
 XX

CC The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the

CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from Wipro at  
 CC ftp.wipro.int/pub/published\_poc\_sequences.  
 CC

SQ Sequence 425 AA;

Query Match 100.0%; Score 1387; DB 7; Length 425;  
 Best Local Similarity 100.0%; Pred No. 2, 1e-99;  
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRAGAACSMRRLRLLLLLIGVSSGAKETCTGLYTHSGECCKACNLGSGVAPCGA 60

Db 1 MRRAGAACSMRRLRLLLLLIGVSSGAKETCTGLYTHSGECCKACNLGSGVAPCGA 60

QY 61 NOTVCEPCLDNVTFSDVVSATPECKPCTECLGLQMSAPCVADAVCRCAVGYODEET 120

Db 61 NOTVCEPCLDNVTFSDVVSATPECKPCTECLGLQMSAPCVADAVCRCAVGYODEET 120

QY 121 GHCEACSVCEVSGVLSGFCODKQNTVCEBCEPGTYSDEANHVDPCLPCTVCEDETEROLRE 180

Db 121 GHCEACSVCEVSGVLSGFCODKQNTVCEBCEPGTYSDEANHVDPCLPCTVCEDETEROLRE 180

QY 181 CTPWADACEEIPGRWIPRSTPEGSDSTAPSTOEPEVPEODLVPSIVADVTTWGS 240

Db 181 CTPWADACEEIPGRWIPRSTPEGSDSTAPSTOEPEVPEODLVPSIVADVTTWGS 240

QY 241 QPVYTRGTTDN 251

Db 241 QPVYTRGTTDN 251

## RESULT 6

ID AAY33483 standard; protein; 427 AA.  
 AAY33483

AC AAY33483;  
 XX

DT 19-JAN-2000 (first entry)  
 XX

DE Human neutrophin receptor p75NTR protein.  
 XX

DE Proapoptotic; dependence domain; p75NTR; androgen receptor; DCC;  
 XX huntingtin polypeptide; Machado-Joseph disease; SCA1; SCA2; SCA6;  
 XX atrophin-1; cell death; apoptosis; Huntington's disease; head trauma;  
 XX Alzheimer's disease; Kennedy's disease; spinocerebellar ataxia; stroke;  
 XX dentatorubropallidoluysian atrophy; cell proliferation; cell survival;  
 XX neoplastic; malignant; autoimmune; fibrotic.  
 XX

OS Homo sapiens.  
 XX

PN WO9945944-A1.  
 XX

PD 16-SEP-1999.  
 XX

PF 11-MAR-1999; 99WO-US005250.  
 XX

PR 12-MAR-1998; 98US-0004186.  
 XX

PA (BURN-) BURNHAM INST.  
 XX

PA Bredesen DE, Rabizadeh S;  
 XX

PI WPI; 1999-561617/47.  
 XX

DR N-PSDB; AA23423.  
 XX

DR N-PSDB; AA23423.  
 XX

XX





KM anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;  
 KM gene therapy; restenosis; graft versus host disease; tumour; cancer;  
 KM apoptotic cell death related disease; autoimmune disorder;  
 KM cardiovascular disorder; viral infection.  
 OS Homo sapiens.  
 XX WO200071150-A1.  
 PN 30-NOV-2000.  
 PD 18-MAY-2000; 2000WO-US013515.  
 PF 20-MAY-1999; 99US-0135164P.  
 PR (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX  
 PI Wei Y, Ruben SM, Gentz RL, Ni J,  
 DR WPI; 2001-041051/05.  
 XX  
 XX Nucleic acid encoding a TRID polypeptide, also referred to as tumor  
 PT necrosis factor receptor 5, useful in the diagnosis, treatment or  
 PT prevention of cancer, autoimmune disorders and viral infection.  
 XX  
 PS Disclosure; Fig 2; 285pp; English.  
 XX  
 XX The present invention describes the human TRID protein (tumour necrosis  
 CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without  
 CC intracellular domain, also referred to as tumour necrosis factor receptor  
 CC 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive, necrotic,  
 CC neuroprotective, antiviral, antiinflammatory, anticonvulsant,  
 CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic  
 CC activities, and can be used in gene therapy. The TRID polynucleotides are  
 CC useful for detecting complementary polynucleotides. TRID proteins and  
 CC polynucleotides are useful in the treatment of tumours, resistance to  
 CC parasite, bacteria and viruses, restenosis and graft versus host disease.  
 CC They are also useful for inducing proliferation of T-cells, endothelial  
 CC cells and certain haematopoietic cells, to regulate antiviral responses  
 CC and to prevent certain autoimmune diseases after stimulation of TRID by  
 CC an agonist or TRAIL binding facilitator. The antibodies which bind TRID  
 CC polypeptides are useful for treating and/or preventing diseases  
 CC associated with increased or decreased apoptotic cell death. The TRID  
 CC polynucleotides, proteins, antibodies, agonists and antagonists are  
 CC useful in the diagnosis, treatment or prevention of: (a) cancer; (b)  
 CC autoimmune disorders; (c) diseases associated with increased apoptosis;  
 CC (d) cardiovascular disorders; and (e) viral infection. The present  
 CC sequence represents a tumour necrosis factor receptor used in comparison  
 CC with TRID in the exemplification of the present invention  
 XX  
 SQ Sequence 427 AA;  
 Query Match 89.7%; Score 1244; DB 4; Length 427;  
 Best Local Similarity 90.7%; Pred. No. 2.6e-88;  
 Matches 225; Conservative 6; Mismatches 17; Indels 0; Gaps 0;  
 QY 4 AGAAGCAMPRLRLILLILGVSSGAKETCSGLYTHSGECKACNLGEGVAOPCGANOT 63  
 DB 3 AGATGRAMDGPRLILLILGVSLGAKACPTGLYTHSGECKACNLGEGVAOPCGANOT 62  
 QY 64 VCEPCLDNTFSDVSVATPECKPCTCTCLGQMSAPCEVADAVRCAGVYQDEBTGHC 123  
 DB 63 VCEPCLDSTFSDVSVATPECKPCTCTCGVLSVAPCEVADAVRCAGVYQDEBTGHC 122  
 QY 124 EACSVCEVSGGLVSCODKONTVCCECPBGITYSDEANHYDPCLPCTVCEDETEROLRECTP 183  
 DB 123 EACRVCBAGSGLVSCODKONTVCCECPBGITYSDEANHYDPCLPCTVCEDETEROLRECTR 182  
 QY 184 WAAABCEETFGRWIPSTPEGSdstAPSTOBEVEPEBODIVPSTADVTTVMSSOPV 243  
 DB 183 WAAABCEETFGRWITSTPEGSdstAPSTOBEVEPEBODIVPSTADVTTVMSSOPV 242  
 QY 244 VTRGTTDN 251

DB 243 VTRGTTDN 250  
 |||||  
 |||||  
 RESULT 9  
 ID AAE21670  
 XX AAE21670 standard; protein; 427 AA.  
 XX  
 AC AAE21670;  
 XX  
 DE 16-JUL-2002 (first entry)  
 XX  
 DE Human neurotrophic receptor (p75NTR) protein.  
 XX  
 KM Human; diabetic neuropathy; therapy; neurotrophic receptor; p75NTR;  
 KM drug screening; receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..28  
 FT /label= Signal\_peptide  
 FT Protein 29..427  
 FT /label= Human\_mature\_p75NTR  
 XX  
 XX WO200218955-A1.  
 XX  
 XX 07-MAR-2002.  
 XX  
 XX 29-AUG-2001; 2001WO-GB003859.  
 XX  
 PR 01-SEP-2000; 2000GB-00021609.  
 XX  
 XX (UTMA-) UNIV VICTORIA MANCHESTER.  
 XX  
 PI Tomlinson DR;  
 DR WPI; 2002-329796/36.  
 XX  
 XX Detecting neuropathy, evaluating effect/efficacy of a drug for treating  
 PT neuropathy or screening compounds to assess their side effects causing  
 PT neuropathy, by detecting 75 kDa Neurotrophic Receptor in patient sample.  
 XX  
 PS Disclosure; Fig 1; 33pp; English.  
 XX  
 XX The invention relates to an in vitro test for neuropathy, for evaluating  
 CC whether a subject will benefit from a putative drug for treating  
 CC neuropathy. The method comprising detecting for the presence of a 75 kDa  
 CC neurotrophic receptor (p75NTR) in a body fluid sample. The invention is  
 CC used for diagnosing neuropathy, particularly diabetic neuropathy,  
 CC screening the efficacy of a putative drug for treating neuropathy, for  
 CC evaluating whether or not a subject will benefit from a putative drug for  
 CC treating neuropathy, for screening a compound to assess whether or not a  
 CC compound causes neuropathy, monitoring the health status of a subject  
 CC with or at risk of developing neuropathy and testing whether or not a  
 CC subject is complying with therapeutic regime for treating diabetes. The  
 CC method is also useful for making a detailed analysis such as a clinical  
 CC trial of a drug targeted at diabetic neuropathy. The present sequence is  
 CC human p75NTR protein  
 XX  
 SQ Sequence 427 AA;  
 Query Match 89.7%; Score 1244; DB 5; Length 427;  
 Best Local Similarity 90.7%; Pred. No. 2.6e-88;  
 Matches 225; Conservative 6; Mismatches 17; Indels 0; Gaps 0;  
 QY 4 AGAAGCAMPRLRLILLILGVSSGAKETCSGLYTHSGECKACNLGEGVAOPCGANOT 63  
 DB 3 AGATGRAMDGPRLILLILGVSLGAKACPTGLYTHSGECKACNLGEGVAOPCGANOT 62  
 QY 64 VCEPCLDNTFSDVSVATPECKPCTCTCLGQMSAPCEVADAVRCAGVYQDEBTGHC 123  
 DB 63 VCEPCLDSTFSDVSVATPECKPCTCTCGVLSVAPCEVADAVRCAGVYQDEBTGHC 122

GenCore version 5.1.6  
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OW protein - protein search, using sw model

Run on: March 12, 2004, 16:28:38 ; Search time 22 seconds  
(without alignments)  
589.005 Million cell updates/sec

Title: US-09-821-831-4  
Perfect score: 1387  
Sequence: 1 MRRAGACSMRRLRLILL.....MTTWGSSQPVTRGTTDN 251

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1387	100.0	425	US-09-748-537-14	Sequence 14, Appl
2	1244	89.7	427	US-09-086-483A-4	Sequence 4, Appl
3	1244	89.7	427	US-09-041-886-2	Sequence 2, Appl
4	1244	89.7	427	US-09-006-353A-5	Sequence 5, Appl
5	1244	89.7	427	US-09-573-986-5	Sequence 5, Appl
6	1244	89.7	427	US-09-580-212-4	Sequence 4, Appl
7	1244	89.7	427	US-09-769-402-4	Sequence 4, Appl
8	1244	89.7	427	US-09-748-537-13	Sequence 13, Appl
9	1244	89.7	427	US-09-527-236A-4	Sequence 4, Appl
10	1244	89.7	427	US-09-756-854-4	Sequence 4, Appl
11	1133	81.7	224	US-08-974-022-50	Sequence 50, Appl
12	1133	81.7	224	US-08-795-445A-50	Sequence 50, Appl
13	1133	81.7	224	US-08-795-447A-50	Sequence 50, Appl
14	1133	81.7	224	US-08-974-186-50	Sequence 50, Appl
15	1133	81.7	224	US-08-795-446B-50	Sequence 50, Appl
16	1133	81.7	224	US-08-708-945D-137	Sequence 137, Appl
17	1133	81.7	224	US-08-577-088C-51	Sequence 51, Appl
18	891	64.2	159	US-08-232-767A-11	Sequence 11, Appl
19	866	62.4	159	US-08-828-683A-16	Sequence 16, Appl
20	858	61.9	159	US-08-219-237B-6	Sequence 6, Appl
21	858	61.9	159	US-08-468-560C-6	Sequence 6, Appl
22	851	61.4	159	US-08-477-347-15	Sequence 15, Appl
23	851	61.4	159	US-08-476-862-6	Sequence 6, Appl
24	851	61.4	159	US-09-800-909-6	Sequence 6, Appl
25	851	61.4	159	US-09-800-908-15	Sequence 15, Appl
26	402	29.0	76	US-08-866-545-4	Sequence 4, Appl
27	402	29.0	76	US-09-627-775-4	Sequence 4, Appl

28	329	23.7	58	3	US-08-904-446A-15	Sequence 15, Appl
29	307	22.1	58	3	US-08-904-446A-14	Sequence 14, Appl
30	270	19.5	58	3	US-08-904-446A-16	Sequence 16, Appl
31	251	18.1	42	1	US-08-050-319B-42	Sequence 42, Appl
32	251	18.1	42	1	US-08-465-982-42	Sequence 42, Appl
33	233	16.8	42	1	US-08-050-319B-33	Sequence 33, Appl
34	233	16.8	42	1	US-08-465-982-33	Sequence 33, Appl
35	231	16.7	40	1	US-08-050-319B-38	Sequence 38, Appl
36	231	16.7	40	1	US-08-465-982-38	Sequence 38, Appl
37	216.5	15.6	277	2	US-08-469-633A-4	Sequence 4, Appl
38	214	15.4	277	2	US-08-147-784-2	Sequence 2, Appl
39	214	15.4	277	3	US-08-195-967-2	Sequence 2, Appl
40	214	15.4	277	3	US-09-006-353A-12	Sequence 12, Appl
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42	214	15.4	277	4	US-09-573-986-12	Sequence 12, Appl
43	214	15.4	277	4	US-09-880-939-2	Sequence 2, Appl
44	214	15.4	277	4	US-09-804-200-2	Sequence 2, Appl
45	211	15.2	419	3	US-08-509-024-7	Sequence 7, Appl

## ALIGNMENTS

RESULT 1  
US-09-748-537-14  
Sequence 14, Application US/09748537  
Patent No. 6680167  
GENERAL INFORMATION:  
APPLICANT: Bertin, John  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILIE AND USES THERE  
FILE REFERENCE: 07334-316001  
CURRENT FILING DATE: 2000-12-26  
CURRENT APPLICATION NUMBER: US/09/748,537  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: US 09/099,041  
PRIOR FILING DATE: 1998-02-06  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14  
LENGTH: 425  
TYPE: PRT  
ORGANISM: Rattus rattus  
US-09-748-537-14

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Best Local Similarity 100.0%; Pred. No. 3.6e-113;  
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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241 QPVVTRGTTDN 251  
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RESULT 2  
US-09-086-483A-4

Sequence 4, Application US/09086483A  
Patent No. 6214580  
GENERAL INFORMATION:  
APPLICANT: NI, et al.  
TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/086,483A  
FILING DATE: May-29-98  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/050,936  
FILING DATE: May-30-97  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/069,112  
FILING DATE: Dec-9-97  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BROOKES, ANDERS A.  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF379  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 427 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-086-483A-4

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Best Local Similarity 90.7%; Pred. No. 1.1e-100;  
Matches 225; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

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DB 63 VCEPCLDNVTFSVDVSAATEPCPCTECLGTQSMASAPCEVADAVCRCAVGYODEETGHC 122  
QY 124 EACSVCEVSGGLVFSQCDKONTVCEBCEGTYSDENAHVDPCLPCTVCEDETERQLRECTR 183  
DB 123 EACRVCEAGSGLVFSQCDKONTVCEBCEGTYSDENAHVDPCLPCTVCEDETERQLRECTR 182  
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QY 244 VTRGTTDN 251  
DB 243 VTRGTTDN 250

RESULT 3  
US-09-041-886-2

Sequence 2, Application US/09041886  
Patent No. 6235872  
GENERAL INFORMATION:  
APPLICANT: Bredesen, Dale E.  
TITLE OF INVENTION: Rabizaden, Sharioz  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/041,886  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 2626  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 427 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-041-886-2

Query Match 89.7%; Score 1244; DB 3; Length 427;  
Best Local Similarity 90.7%; Pred. No. 1.1e-100;  
Matches 225; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 4 AGAACSAMDRLRLILLILGVSSGGAKECTSTGLYTHSGECCKACNLGEGVAQPCGANOT 63  
DB 3 AGATGRAMDPRILLILLIGVSLGGAKEACPTGLYTHSGECCKACNLGEGVAQPCGANOT 62  
QY 64 VCEPCLDNVTFSVDVSAATEPCPCTECLGTQSMASAPCEVADAVCRCAVGYODEETGHC 123  
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QY 244 VTRGTTDN 251  
DB 243 VTRGTTDN 250

RESULT 4  
US-09-006-353A-5  
Sequence 5, Application US/09006353A  
Patent No. 6261801  
GENERAL INFORMATION:  
APPLICANT: MEI, YING-FEI  
APPLICANT: YU, GUO-LIANG  
APPLICANT: GENTZ, REINER  
APPLICANT: RUBEN, STEVEN



Db 183 WADACEEIPGRWITRSTPEGSDSTAPSTQEPPEAPPEODLIASIVAGVTTWSSQPV 242  
QY 244 VTRGTTDN 251  
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## RESULT 7

US-09-769-402-4  
Sequence 4, Application US/09769402  
Patent No. 6607726  
GENERAL INFORMATION:  
APPLICANT: NI, et al.  
TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/769,402  
FILING DATE: 26-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/086,483  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 60/069,112  
FILING DATE: Dec-9-97  
ATTORNEY/AGENT INFORMATION:  
NAME: BROOKES, ANDERS A.  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF379  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 427 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-769-402-4

Query Match 89.7%; Score 1244; DB 4; Length 427;  
Best Local Similarity 90.7%; Pred. No. 1.1e-100;  
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Db 183 WADACEEIPGRWITRSTPEGSDSTAPSTQEPPEAPPEODLIASIVAGVTTWSSQPV 242

QY 244 VTRGTTDN 251  
Db 243 VTRGTTDN 250

## RESULT 8

US-09-748-537-13  
Sequence 13, Application US/09748537  
Patent No. 6680167  
GENERAL INFORMATION:  
APPLICANT: Bertin, John  
APPLICANT: Chao, Moses V.  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILIE AND USES THERE  
FILE REFERENCE: 07334-316001  
CURRENT APPLICATION NUMBER: US/09/748,537  
CURRENT FILING DATE: 2000-12-26  
PRIOR APPLICATION NUMBER: US 09/099,041  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: US 09/019,942  
PRIOR FILING DATE: 1998-02-06  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 427  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-748-537-13

Query Match 89.7%; Score 1244; DB 4; Length 427;  
Best Local Similarity 90.7%; Pred. No. 1.1e-100;  
Matches 225; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

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Db 243 VTRGTTDN 250

## RESULT 9

US-09-527-236A-4  
Sequence 4, Application US/09527236A  
Patent No. 6358508  
GENERAL INFORMATION:  
APPLICANT: NI, Jian  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Fan, Ping  
APPLICANT: Gentz, Reiner L.  
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9  
FILE REFERENCE: PF375P1  
CURRENT APPLICATION NUMBER: US/09/527,236A  
CURRENT FILING DATE: 2000-03-16  
PRIOR APPLICATION NUMBER: 60/052,991  
PRIOR FILING DATE: 1997-06-11  
PRIOR APPLICATION NUMBER: 09/095,094  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/126,019  
PRIOR FILING DATE: 1999-03-24

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

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Title: US-09-821-831-4

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Listing first 45 summaries

Database : Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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6	1244	89.7	427	9	US-09-748-537-13
7	1244	89.7	427	9	US-09-935-727-7
8	1244	89.7	427	11	US-09-230-111C-24
9	1244	89.7	427	14	US-10-155-886-5
10	1244	89.7	427	14	US-10-186-543-5
11	1244	89.7	427	14	US-10-092-138-24
12	1244	89.7	427	14	US-10-280-047-4
13	1244	89.7	427	15	US-10-418-242-7
14	1244	89.7	455	9	US-09-756-854-4
15	1244	89.7	455	13	US-10-041-574-4

16	1133	81.7	224	11	US-09-405-032-134	Sequence 134, App
17	866	62.4	159	13	US-10-112-793-16	Sequence 16, Appl
18	858	61.9	159	9	US-09-884-987-6	Sequence 6, Appl1
19	851	61.4	159	9	US-09-800-909-6	Sequence 6, Appl1
20	851	61.4	159	9	US-09-800-908-15	Sequence 15, Appl1
21	851	61.4	159	15	US-10-423-927-6	Sequence 6, Appl1
22	214	15.4	274	9	US-09-836-607-3	Sequence 3, Appl1
23	214	15.4	274	10	US-09-421-112-3	Sequence 3, Appl1
24	214	15.4	277	9	US-09-825-213-12	Sequence 12, Appl1
25	214	15.4	277	9	US-09-852-845-2	Sequence 2, Appl1
26	214	15.4	277	9	US-09-804-200-2	Sequence 2, Appl1
27	214	15.4	277	9	US-09-800-939-2	Sequence 2, Appl1
28	214	15.4	277	9	US-09-768-779A-5	Sequence 5, Appl1
29	214	15.4	277	9	US-09-935-727-14	Sequence 14, Appl1
30	214	15.4	277	14	US-10-140-164-6	Sequence 6, Appl1
31	214	15.4	277	14	US-10-046-433-3	Sequence 3, Appl1
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33	214	15.4	277	14	US-10-186-643-12	Sequence 5, Appl1
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35	214	15.4	277	14	US-10-073-333A-6	Sequence 6, Appl1
36	214	15.4	277	14	US-10-326-929-2	Sequence 2, Appl1
37	214	15.4	277	15	US-10-323-274C-2	Sequence 2, Appl1
38	214	15.4	277	15	US-10-418-242-14	Sequence 7, Appl1
39	211	15.2	419	9	US-09-924-231-7	Sequence 4, Appl1
40	210	15.1	276	15	US-10-369-300-4	Sequence 18, Appl1
41	208	15.0	197	9	US-09-934-289A-18	Sequence 2, Appl1
42	207	14.9	444	14	US-10-363-447-2	Sequence 4, Appl1
43	205.5	14.8	909	14	US-10-226-296-4	Sequence 4, Appl1
44	205.5	14.8	909	14	US-10-226-318-4	Sequence 4, Appl1
45	204.5	14.7	336	9	US-09-756-166-8	Sequence 8, Appl1

## ALIGNMENTS

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RESULT 1
US-09-821-831-4
: Sequence 4, Application US/09821831
: Patent No. US20020137188A1
: GENERAL INFORMATION:
: APPLICANT: Bartlett, Perry Francis
: APPLICANT: Coulson, Elizabeth Jane
: APPLICANT: Fieldew, Katrina
: APPLICANT: Baca, Manuel
: APPLICANT: Kilpatrick, Trevor
: APPLICANT: Surindat, Cheema
: TITLE OF INVENTION: Method of Modulating Cell Survival and
: FILE REFERENCE: 3206.1001-000
: CURRENT APPLICATION NUMBER: US/09/821,831
: CURRENT FILING DATE: 2001-03-30
: PRIOR APPLICATION NUMBER: PCT/AU99/00860
: PRIOR FILING DATE: 1999-10-05
: PRIOR APPLICATION NUMBER: AU PQ0701
: PRIOR FILING DATE: 1999-06-01
: PRIOR APPLICATION NUMBER: AU PP6351
: PRIOR FILING DATE: 1998-10-07
: PRIOR APPLICATION NUMBER: AU PP6353
: PRIOR FILING DATE: 1998-10-06
: NUMBER OF SEQ ID NOS: 72
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 251
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Deduced amino acid sequence
US-09-821-831-4
Query Match 100.0% Score 1387; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.3e-107;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MRAGAACSAMDRLRLILLILGVSSGAKETCTGLYTHSGECCCKACNLGEGVAQPCGA 60  
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DB 181 CTPMADACEEIPGRWIPRSTPPEGSSTAPSTQEPPEVPEODLVSTVADMTVTWSS 240  
QY 241 QPVVTRGTTDN 251  
DB 241 QPVVTRGTTDN 251

## RESULT 2

US-09-748-537-14  
Sequence 14, Application US/09748537  
Patent No. US20020061833A1  
GENERAL INFORMATION:  
APPLICANT: Bertin, John  
APPLICANT: Chao, Moses V.  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILIE AND USES THERE  
FILE REFERENCE: 07334-316001  
CURRENT APPLICATION NUMBER: US/09/748,537  
CURRENT FILING DATE: 2000-12-26  
PRIOR APPLICATION NUMBER: US 09/099,041  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: US 09/019,942  
PRIOR FILING DATE: 1998-02-06  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14  
LENGTH: 425  
TYPE: PRT  
ORGANISM: Rattus rattus  
US-09-748-537-14

Query Match 100.0%; Score 1387; DB 9; Length 425;  
Best Local Similarity 100.0%; Pred. No. 2,3e-107;  
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAGAACSAMDRLRLILLILGVSSGAKETCTGLYTHSGECCCKACNLGEGVAQPCGA 60  
DB 1 MRAGAACSAMDRLRLILLILGVSSGAKETCTGLYTHSGECCCKACNLGEGVAQPCGA 60  
QY 61 NOTVCEPCLDNVTFSDVVSATPECKPCTECLGLQSMAPCVEADDAVCRAVGYQDEET 120  
DB 61 NOTVCEPCLDNVTFSDVVSATPECKPCTECLGLQSMAPCVEADDAVCRAVGYQDEET 120  
QY 121 GHGACACVCEVSGSLVSCODKONTVCECEPCEGTYSDEANHVDPCLPCTVCEDETERQLE 180  
DB 121 GHGACACVCEVSGSLVSCODKONTVCECEPCEGTYSDEANHVDPCLPCTVCEDETERQLE 180  
QY 181 CTPMADACEEIPGRWIPRSTPPEGSSTAPSTQEPPEVPEODLVSTVADMTVTWSS 240  
DB 181 CTPMADACEEIPGRWIPRSTPPEGSSTAPSTQEPPEVPEODLVSTVADMTVTWSS 240  
QY 241 QPVVTRGTTDN 251  
DB 241 QPVVTRGTTDN 251

RESULT 3  
US-09-821-831-2  
Sequence 2, Application US/09821831  
Patent No. US20020137188A1

GENERAL INFORMATION:  
APPLICANT: Bertin, Perry Francis  
APPLICANT: Coulson, Elizabeth Jane  
APPLICANT: Fielder, Katrina  
APPLICANT: Baca, Manuel  
APPLICANT: Kilpatrick, Trevor  
APPLICANT: Surindar, Cheema  
TITLE OF INVENTION: Method of Modulating Cell Survival and  
FILE REFERENCE: 3206-1001-000  
CURRENT APPLICATION NUMBER: US/09/821,831  
CURRENT FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: PCT/AU99/00860  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: AU PQ0701  
PRIOR FILING DATE: 1999-06-01  
PRIOR APPLICATION NUMBER: AU PP6351  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: AU PP6353  
PRIOR FILING DATE: 1998-10-06  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 425  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Deduced amino acid sequence  
US-09-821-831-2

Query Match 100.0%; Score 1387; DB 9; Length 425;  
Best Local Similarity 100.0%; Pred. No. 2,3e-107;  
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAGAACSAMDRLRLILLILGVSSGAKETCTGLYTHSGECCCKACNLGEGVAQPCGA 60  
DB 1 MRAGAACSAMDRLRLILLILGVSSGAKETCTGLYTHSGECCCKACNLGEGVAQPCGA 60  
QY 61 NOTVCEPCLDNVTFSDVVSATPECKPCTECLGLQSMAPCVEADDAVCRAVGYQDEET 120  
DB 61 NOTVCEPCLDNVTFSDVVSATPECKPCTECLGLQSMAPCVEADDAVCRAVGYQDEET 120  
QY 121 GHGACACVCEVSGSLVSCODKONTVCECEPCEGTYSDEANHVDPCLPCTVCEDETERQLE 180  
DB 121 GHGACACVCEVSGSLVSCODKONTVCECEPCEGTYSDEANHVDPCLPCTVCEDETERQLE 180  
QY 181 CTPMADACEEIPGRWIPRSTPPEGSSTAPSTQEPPEVPEODLVSTVADMTVTWSS 240  
DB 181 CTPMADACEEIPGRWIPRSTPPEGSSTAPSTQEPPEVPEODLVSTVADMTVTWSS 240  
QY 241 QPVVTRGTTDN 251  
DB 241 QPVVTRGTTDN 251

## RESULT 4

US-08-681-219-26  
Sequence 26, Application US/08681219  
Patent No. US20020058607A1  
GENERAL INFORMATION:  
APPLICANT: Takaki, Sato and Junn Yanagisawa  
TITLE OF INVENTION: COMPOUNDS THAT INHIBIT THE INTERACTION BETWEEN  
TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GPCR  
TITLE OF INVENTION: (PDZ/DHR) DOMAIN AND USES THEREOF  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:



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OM protein - protein search, using SW model

Run on: March 12, 2004, 16:27:22 ; Search time 18 seconds  
(without alignments)

726.089 Million cell updates/sec

Title: US-09-821-831-4

Sequence: 1 MRAAGACGANDRLRLLL.....MTTWGSSQPVTRGTTDN 251

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1397	100.0	425	TR16_RAT	P01714 ratu
2	1247	89.9	417	TR16_MOUSE	Q970W1 mus muscu
3	1244	89.7	427	TR16_HUMAN	P08138 homo sapien
4	883.5	63.7	416	TR16_CHICK	P18519 gallu
5	215.5	15.5	461	TR1A_RAT	P22934 ratu
6	214	15.4	277	TR1A_HUMAN	P43489 homo sapien
7	211	15.2	204	TR26_MOUSE	P83626 mus muscu
8	203.5	14.7	283	TR14_HUMAN	Q92956 homo sapien
9	202	14.6	289	TR16_MOUSE	P27512 mus muscu
10	197.5	14.2	454	TR1A_MOUSE	P25118 mus muscu
11	197.5	14.2	455	TR1A_HUMAN	P15438 homo sapien
12	196.5	14.2	325	VT2_SPYKA	P25943 shope fibro
13	194	14.0	401	TR1B_MOUSE	O08712 mus muscu
14	193.5	14.0	326	VT2_MXVXL	P23825 myxoma viru
15	191.5	13.8	259	TR1C_HUMAN	O14798 h tumor nec
16	189.5	13.7	271	TR1A_RAT	P15725 ratu
17	189.5	13.7	401	TR1B_HUMAN	O03000 homo sapien
18	188	13.6	471	TR1A_BOVIN	O15131 bos tauru
19	186.5	13.4	472	TR1A_MOUSE	P50284 mus muscu
20	183	13.2	415	TR1A_MOUSE	O75509 homo sapien
21	181	13.0	655	TR1A_HUMAN	P25119 mus muscu
22	180.5	13.0	474	TR1B_MOUSE	Q96PUS mus muscu
23	176	12.7	655	TR1A_MOUSE	P25942 homo sapien
24	175.5	12.7	277	TR1B_HUMAN	Q96P62 mus muscu
25	175	12.6	198	TR1A_HUMAN	O36941 homo sapien
26	175	12.6	435	TR1A_MOUSE	O08727 ratu
27	173	12.5	401	TR1B_RAT	O08727 ratu
28	171.5	12.4	3075	TR1A_HUMAN	Q96P61 homo sapien
29	171	12.3	176	TR1A_MOUSE	Q96P61 mus muscu
30	171	12.3	461	TR1A_PIG	P50555 sus scrofa
31	170.5	12.3	461	TR1B_HUMAN	P20363 homo sapien
32	170.5	12.3	616	TR1A_HUMAN	Q96P62 mus muscu
33	168	12.1	300	TR1B_HUMAN	O95407 homo sapien

## ALIGNMENTS

RESULT 1	ID	TR16_RAT	STANDARD;	PRT;	425 AA.
AC	P01714;				
DT	01-APR-1988 (Rel. 07, Created)				
DT	01-APR-1988 (Rel. 07, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	Tumor necrosis factor receptor superfamily member 16 precursor (low-affinity nerve growth factor receptor) (NGF receptor) (p75 <sup>NTR</sup> ) (p75 <sup>ICD</sup> ) (low affinity neurotrophin receptor p75 <sup>NTR</sup> )				
GN	NGFR OR TNFRSF16.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=87115859; PubMed=3027580;				
RA	Radeke M.J., Misko T.P., Hsu C., Herzberg L.A., Shooter E.M.;				
RT	"Gene transfer and molecular cloning of the rat nerve growth factor receptor.";				
RL	Nature 325:593-597(1987).				
RN	[2]				
RP	SEQUENCE OF 1-22 FROM N.A.				
RC	TISSUE=Liver;				
RX	MEDLINE=93077038; PubMed=1446821;				
RA	Medsis M., Timmusk T., Allkneis R., Saarna M., Persson H.;				
RT	"Regulatory elements and transcriptional regulation by testosterone and retinoic acid of the rat nerve growth factor receptor promoter.";				
RL	Gene 121:247-254(1992).				
RN	[3]				
RP	STRUCTURE BY NMR OF 334-418.				
RX	MEDLINE=97449145; PubMed=9305641;				
RA	Liepinsh E., Ilag L.L., Oetting G., Ibanez C.F.;				
RT	"NMR structure of the death domain of the p75 neurotrophin receptor.";				
RL	EMBO J. 16:4999-5005(1997).				
CC	-1- FUNCTION: low affinity receptor which can bind to NGF, BDNF, NT-3, and NT-4. Can mediate cell survival as well as cell death of neural cells.				
CC	-1- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75 <sup>NTR</sup> associated cell death executor. Interacts with TRAF2, TRAF4, TRAF6 and PRIP-3 (By similarity).				
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-1- PTM: N- and O-glycosylated.				
CC	-1- PPM: Phosphorylated on serine residues.				
CC	-1- SIMILARITY: Contains 4 TNFR-Cys repeats.				
CC	-1- SIMILARITY: Contains 1 death domain.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				

DR EMBL; X05137; CA28783.1; -  
 DR EMBL; X61269; -; NOT\_ANNOTATED\_CDS.  
 DR PIR; A26431; A26431.  
 DR PDB; INGR; 29-JUL-97.  
 DR InterPro; IPR000468; Death.  
 DR InterPro; IPR01368; TNFR\_c6.  
 DR Pfam; PF00531; death; 1.  
 DR SMART; PF00020; TNFR\_c6; 4.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00208; TNFR; 3.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS00650; TNFR\_NGFR\_2; 4.  
 DR PROSITE; PS0017; DEATH\_DOMAIN; 1.  
 DR Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;  
 Receptor; Phosphorylation; Signal; 3D-structure.  
 FT SIGNAL 1 29  
 FT CHAIN 30 425  
 FT DOMAIN 30 251  
 FT TRANSMEM 252 273  
 FT DOMAIN 274 425  
 FT REPEAT 32 65  
 FT REPEAT 67 108  
 FT REPEAT 109 147  
 FT REPEAT 149 189  
 FT DOMAIN 354 419  
 FT DISULFID 198 249  
 FT DISULFID 33 44  
 FT DISULFID 45 58  
 FT DISULFID 48 65  
 FT DISULFID 68 84  
 FT DISULFID 87 100  
 FT DISULFID 90 108  
 FT DISULFID 110 123  
 FT DISULFID 126 139  
 FT DISULFID 129 147  
 FT DISULFID 150 165  
 FT DISULFID 168 181  
 FT DISULFID 171 189  
 FT CARBOHYD 61 64  
 FT CARBOHYD 71 71  
 SQ SEQUENCE 425 AA; 45432 MW; B2E152D94D3827F8 CRC64;  
 Query Match 100.0%; Score 1387; DB 1; Length 425;  
 Best Local Similarity 100.0%; Pred. No. 7,8e-99;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRAGAACAMDFLRLLILLIIVSSGGAKECTSTGLYTHSGECCKACNLGAGVAPQCA 60  
 DB 1 MRRAGAACAMDFLRLLILLIIVSSGGAKECTSTGLYTHSGECCKACNLGAGVAPQCA 60  
 QY 61 NOTVCEPCLDNVPFSDVSAATEPCCTECLGLQSVAPCEADPAVCAAGYODEET 120  
 DB 61 NOTVCEPCLDNVPFSDVSAATEPCCTECLGLQSVAPCEADPAVCAAGYODEET 120  
 QY 121 GHCEACVCEVSGGLVFCQDKONTVCEGPCBGTVDENAHVDPCLPCTVCEDETEROLKE 180  
 DB 121 GHCEACVCEVSGGLVFCQDKONTVCEGPCBGTVDENAHVDPCLPCTVCEDETEROLKE 180  
 QY 121 GHCEACVCEVSGGLVFCQDKONTVCEGPCBGTVDENAHVDPCLPCTVCEDETEROLKE 180  
 DB 121 GHCEACVCEVSGGLVFCQDKONTVCEGPCBGTVDENAHVDPCLPCTVCEDETEROLKE 180  
 QY 181 CTFWAAACEEIPGRMTPESTPEGSDDTAPSTQSEVEVEPEODLVSTVADAVTTVMGSS 240  
 DB 181 CTFWAAACEEIPGRMTPESTPEGSDDTAPSTQSEVEVEPEODLVSTVADAVTTVMGSS 240  
 QY 241 QPVVTRGTDTN 251  
 DB 241 QPVVTRGTDTN 251

RESULT 2  
 ID TR16\_MOUSE STANDARD; PRT; 417 AA.  
 AC Q9Z0M1;  
 DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 16 precursor (low-  
 DE affinity nerve growth factor receptor) (NGF receptor) (low affinity  
 DE neurotrophin receptor p75NTR).  
 GN NGF OR TNFRSF16.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A;  
 RX MEDLINE=99077793; PubMed=9857182;  
 RA Tuffreau C., Benejean J., Blondel D., Kieffer B., Flament A.;  
 RT "Low-affinity nerve-growth factor receptor (p75NTR) can serve as a  
 RT receptor for rabies virus.";  
 RL EMO J. 17:7250-7259(1998).  
 CC -1- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,  
 CC AND NT-4. Can mediate cell survival as well as cell death of  
 CC neural cells (by similarity). Binds to rabies virus glycoprotein  
 CC Gs.  
 CC -1- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-  
 CC associated cell death executor. Interacts with TRAF2, TRAF4,  
 CC TRAF6 and TRPM3 (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).  
 CC -1- PTM: N- and O-glycosylated (by similarity).  
 CC -1- PTM: Phosphorylated on serine residues (by similarity).  
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC -1- SIMILARITY: Contains 1 death domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL; AF105292; AAD17943.1; -  
 DR HSSP; P07174; INGR.  
 DR MSD; MGI:97323; NGfr.  
 DR GO; GO:0005035; F:death receptor activity; IDA.  
 DR GO; GO:0005035; F:protein binding; IPI.  
 DR GO; GO:0007411; P:axon guidance; IMP.  
 DR GO; GO:0007417; P:central nervous system development; IMP.  
 DR GO; GO:0006917; P:induction of apoptosis; IDA.  
 DR InterPro; IPR000468; Death.  
 DR InterPro; IPR01368; TNFR\_c6.  
 DR Pfam; PF00531; death; 1.  
 DR SMART; PF00020; TNFR\_c6; 4.  
 DR SMART; SM00005; DEATH; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS00650; TNFR\_NGFR\_2; 4.  
 DR PROSITE; PS0017; DEATH\_DOMAIN; 1.  
 DR Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;  
 DR Receptor; Phosphorylation; Signal; 3D-structure.  
 FT SIGNAL 1 21  
 FT CHAIN 22 417  
 FT DOMAIN 22 246  
 FT TRANSMEM 247 265  
 FT DOMAIN 266 417  
 FT REPEAT 24 57  
 FT REPEAT 59 100  
 FT REPEAT 101 139  
 FT REPEAT 141 181  
 FT REPEAT 144 411  
 FT DOMAIN 346 411  
 FT DISULFID 190 241  
 FT DISULFID 25 36  
 FT DISULFID 37 50  
 FT DISULFID 57 57

BY SIMILARITY.  
 TUMOR NECROSIS FACTOR RECEPTOR  
 SUPERFAMILY MEMBER 16.  
 EXTRACELLULAR (POTENTIAL).  
 POTENTIAL.  
 CYTOPLASMIC (POTENTIAL).  
 TNFR-CYS 1.  
 TNFR-CYS 2.  
 TNFR-CYS 3.  
 TNFR-CYS 4.  
 DEATH.  
 SER/THR-RICH.  
 BY SIMILARITY.  
 BY SIMILARITY.  
 BY SIMILARITY.

FT DISULFID 60 76 BY SIMILARITY.  
 FT DISULFID 79 92 BY SIMILARITY.  
 FT DISULFID 82 100 BY SIMILARITY.  
 FT DISULFID 102 115 BY SIMILARITY.  
 FT DISULFID 118 131 BY SIMILARITY.  
 FT DISULFID 121 139 BY SIMILARITY.  
 FT DISULFID 142 157 BY SIMILARITY.  
 FT DISULFID 160 173 BY SIMILARITY.  
 FT DISULFID 163 181 BY SIMILARITY.  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 417 AA; 44666 MW; 5D7A4510DB8AF9B2 CXC64;  
 Query Match 89.9%; Score 1247; DB 1; Length 417;  
 Best Local Similarity 92.6%; Pred. No. 3.6e-88;  
 Matches 225; Conservative 6; Mismatches 10; Indels 2; Gaps 1;  
 QY 11 MDRLR-LLLLLIIGVSSGSGAKETGSLYTHSGCCCAKGLGAGVAPCCANQTVCEPC 68  
 DB 1 MDRLRLLLLLLLVGSGVFGAKETGSLYTHSGCCCAKGLGAGVAPCCANQTVCEPC 60  
 QY 69 LDNTVPSDVATGATEPCCKPCTECLGQSNAPCEVADAVCAVGYQDEBTGCEACSV 128  
 DB 61 LDVTFPSDVATGATEPCCKPCTECLGQSNAPCEVADAVCAVGYQDEBTGCEACSV 120  
 QY 129 CEVSGVGFSCODKNTVCEPCPBTGSDENANHTDPCLPCTVCEDTROLECPMADAE 188  
 DB 121 CGVSGVGFSCODKNTVCEPCPBTGSDENANHTDPCLPCTVCEDTROLECPMADAE 180  
 QY 189 CEETPGRWIPRSTPEGSSTAPSTOBEVPEODLVPSTVADVTTVMSSQPVVTRGT 248  
 DB 181 CEETPGRWIPRSTPEGSSTAPSTOBEVPEODLVPSTVADVTTVMSSQPVVTRGT 240  
 QY 249 TDN 251  
 DB 241 ADN 243  
 Db  
 RESULT 3  
 TR16 HUMAN STANDARD; PRT; 427 AA.  
 ID TR16 HUMAN  
 AC P08138;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 16 precursor (low-affinity nerve growth factor receptor) (NGF receptor) (p80-LNGFR)  
 DE (p75 ICD) (Low affinity neurotrophin receptor p75NTR).  
 OS NGFR OR TNFRSF16.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 EX MEDLINE=87051725; PubMed=3022937;  
 RA Johnson D., Lannan A., Buck C.R., Sehgal A., Morgan C., Mercer E., Bothe M., Chao M.;  
 RT "Expression and structure of the human NGF receptor";  
 RL Cell 47:545-554(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 EX MEDLINE=22386257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F., Datchenko L., Marsiska K., Farmer A.A., Rubin G.M., Hong L., Stjepic M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ueda T.B., Tomihata S., Carninci P., Prange C., Rana S.S., Lochuano N.A., Peters G.J., Abramson R.D., Mullen S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Rahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.N., Krzywicki M.J., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [3]  
 RP SEQUENCE OF 1-22 FROM N.A.  
 RX MEDLINE=8906903; PubMed=2850481;  
 RA Sehgal A., Patil N., Chao M.;  
 RT "A constitutive promoter directs expression of the nerve growth factor receptor gene";  
 RL Mol. Cell. Biol. 8:3160-3167(1988).  
 RN [4]  
 RP INTERACTION WITH TRAF2, TRAF4 AND TRAF6.  
 RX MEDLINE=9944585; PubMed=10514511;  
 RA Ye X., Mehlen P., Rabizadeh S., VanArsdale T., Zhang H., Shin H., Reed J.C., Leo E., Zapata J.M., Hauser C.A., Reed J.C., Bredesen D.E.;  
 RT "TRAF family proteins interact with the common neurotrophin receptor and modulate apoptosis induction";  
 RL J. Biol. Chem. 274:30202-30208(1999).  
 RN [5]  
 RP INTERACTION WITH TRAF6.  
 RX MEDLINE=99115593; PubMed=9915784;  
 RA Khuriedara G., Orlicki J.R., Chao M.V.;  
 RT "Association of the p75 neurotrophin receptor with TRAF6";  
 RL J. Biol. Chem. 274:2597-2600(1999).  
 RN [6]  
 RP INTERACTION WITH PTEN13.  
 RX MEDLINE=20012928; PubMed=10544233;  
 RA Irie S., Hachiya T., Rabizadeh S., Maruyama W., Mukai J., Li Y., Reed J.C., Bredesen D.E., Sato T.A.;  
 RT "Functional interaction of Fas-associated phosphatase-1 (FAP-1) with p75(NTR) and their effect on NF-kappa activation";  
 RL FEBS Lett. 460:191-198(1999).  
 CC -1- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3, and NT-4. Can mediate cell survival as well as cell death of neural cells.  
 CC -1- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-associated cell death executor. Interacts with TRAF2, TRAF4, TRAF6 and PTEN13.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- PTM: N- and O-glycosylated.  
 CC -1- PTM: Phosphorylated on serine residues.  
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC -1- SIMILARITY: Contains 1 death domain.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-eb.ch/announce/> or send an email to [license@isb-eb.ch](mailto:license@isb-eb.ch)).  
 CC  
 DR EMBL; M14764; AA559544.1;  
 DR EMBL; BC050309; AAH50309.1;  
 DR EMBL; M21621; AAA36363.1;  
 DR PIR; A25218; GOHUN.  
 DR HSSP; P07174; INGR.  
 DR Genew; HGNC:7809; NGFR.  
 DR MIM; 162010;  
 DR CO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR CO; GO:0004888; F:transmembrane receptor activity; TAS.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00531; death\_1.  
 DR Pfam; PF00020; TNFR\_c6; 4.  
 DR SMART; SM00005; DEATH; 1.

DR SMART; SMO0208; TNFR; 3.  
 DR PROSITE; PS00652; TNFR\_NGR\_1; 3.  
 DR PROSITE; PS00650; TNFR\_NGR\_2; 4.  
 DR PROSITE; PS00651; DEATH\_DOMAIN; 1.  
 DR Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;  
 KM Repeat; Phosphorylation; Signal.  
 FT SIGNAL 1 28  
 FT CHAIN 29 427  
 FT DOMAIN 29 427  
 FT TRANSMEM 29 427  
 FT REPEAT 31 64  
 FT REPEAT 66 107  
 FT REPEAT 108 146  
 FT REPEAT 149 188  
 FT DOMAIN 344 421  
 FT DOMAIN 197 248  
 FT DISULFID 32 43  
 FT DISULFID 44 57  
 FT DISULFID 47 64  
 FT DISULFID 67 83  
 FT DISULFID 86 99  
 FT DISULFID 89 107  
 FT DISULFID 109 122  
 FT DISULFID 125 138  
 FT DISULFID 128 146  
 FT DISULFID 149 164  
 FT DISULFID 167 180  
 FT DISULFID 170 188  
 FT CARBOHYD 60 60  
 SQ SEQUENCE 427 AA; 45183 MW; B09FAL3FB5D625B CRC64;  
 N-LINKED (GLCNAC...) (POTENTIAL).  
 Query Match 89.7%; Score 1244; DB 1; Length 427;  
 Best Local Similarity 90.7%; Pred. No. 6,2e-68;  
 Matches 225; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 4 AGAACSMRDLRLILLILGVSSGAKETSTGLYHSGECCKACNLGEGVAPGCGANT 63  
 DB 3 AGATGRMDPRLILLILGVSSGAKETSTGLYHSGECCKACNLGEGVAPGCGANT 62  
 QY 64 VCEPCLDNTVTSVDVATEPCPCCTECLGLQSMADPCVADAVCAAGYQDEETGHC 123  
 DB 63 VCEPCLDNTVTSVDVATEPCPCCTECLGLQSMADPCVADAVCAAGYQDEETGHC 122  
 QY 124 EACSVCEVSGGLVFSQCDKQNTVCEPCPGTISDANHYDPCLPCTVCECTERQRECEP 183  
 DB 123 EACSVCEVSGGLVFSQCDKQNTVCEPCPGTISDANHYDPCLPCTVCECTERQRECEP 182  
 QY 184 WADACEEIPGRWIPRSTPEGSSTAPSTOEPEVPEPDQLVSTVADVTTVMGSSOPV 243  
 DB 183 WADACEEIPGRWIPRSTPEGSSTAPSTOEPEVPEPDQLVSTVADVTTVMGSSOPV 242  
 QY 244 VTRGTTDN 251  
 DB 243 VTRGTTDN 250

RESULT 4  
 TR16\_CHICK STANDARD; PRT; 416 AA.  
 ID TR16\_CHICK STANDARD; PRT; 416 AA.  
 AC P18519;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 16 precursor (Low-affinity nerve growth factor receptor) (Gp80-LNGR)  
 DE (D75 ICD) (low affinity neurotrophin receptor p75NTR).  
 GN NGFR OR TNFRSF16.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OX NGR\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=90166579; PubMed=2560385;  
 RA Large T.H., Weskamp G., Helder J.C., Radeke M.J., Misko T.P.,  
 RA Shooter E.M., Reichardt L.F.;  
 RT "Structure and developmental expression of the nerve growth factor receptor in the chicken central nervous system";  
 RL Neuron 2:1123-1134(1989).  
 RN [2]  
 RP SEQUENCE OF 21-416 FROM N.A.  
 RX MEDLINE=90152140; PubMed=2154393;  
 RA Heuer J.G., Falemie-Nantie S., Wheeler E.F., Bothwell M.;  
 RT "Structure and developmental expression of the chicken NGF receptor";  
 RL Dev. Biol. 137:287-304(1990).  
 CC -1- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3, and NT-4. Can mediate cell survival as well as cell death of neural cells (By similarity).  
 CC -1- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-associated cell death executor. Interacts with TRAF2, TRAF3, TRAF6 and p19N13 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- PTM: N- and O-glycosylated.  
 CC -1- PTM: Phosphorylated on serine residues.  
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC -1- SIMILARITY: Contains 1 death domain.  
 DR PIR; J00006; J00006.  
 DR HSSP; P07174; INGR.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00531; death; 1.  
 DR Pfam; PF00020; TNFR\_c6; 4.  
 DR SMART; SMO0005; DEATH; 1.  
 DR SMART; SMO0208; TNFR; 3.  
 DR PROSITE; PS00652; TNFR\_NGR\_1; 3.  
 DR PROSITE; PS00650; TNFR\_NGR\_2; 3.  
 DR PROSITE; PS00651; DEATH\_DOMAIN; 1.  
 DR Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;  
 KM Repeat; Phosphorylation; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 416  
 FT DOMAIN 29 416  
 FT TRANSMEM 29 416  
 FT REPEAT 23 57  
 FT REPEAT 58 99  
 FT REPEAT 100 138  
 FT REPEAT 140 180  
 FT DOMAIN 333 410  
 FT DOMAIN 188 236  
 FT DISULFID 24 35  
 FT DISULFID 36 49  
 FT DISULFID 39 56  
 FT DISULFID 59 75  
 FT DISULFID 78 91  
 FT DISULFID 81 99  
 FT DISULFID 101 114  
 FT DISULFID 117 130  
 FT DISULFID 120 138  
 FT DISULFID 141 156  
 FT DISULFID 159 172  
 FT DISULFID 162 180  
 FT CARBOHYD 52 52  
 FT CONFLICT 36 36  
 FT CONFLICT 173 173  
 FT CONFLICT 276 276  
 FT CONFLICT 396 396  
 SQ SEQUENCE 416 AA; 44654 MW; 6BCEAB4FAD2D56 CRC64;  
 Query Match 63.7%; Score 883.5; DB 1; Length 416;  
 Best Local Similarity 66.1%; Pred. No. 1.8e-60;

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 12, 2004, 16:27:22 ; Search time 45 Seconds

(without alignments)  
1759.890 Million cell updates/sec

Title: US-09-821-831-4

Sequence: 1 MRACAGACASMDRLRLDLLL.....MTTWGSSQPVVTRGTTDN 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SEPREMBL 25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriaph:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1297	93.5	427	11	Q8CFT3 Q8CFT3 mus musculi
2	1247	89.9	417	11	Q8BYX1 Q8BYX1 mus musculi
3	619.5	44.7	401	13	Q9PRG7 Q9PRG7 xenopus lae
4	523	37.7	317	13	Q8FV6 Q8FV6 brachydanio
5	420	30.3	387	13	Q9PV4 Q9PV4 xenopus lae
6	381.5	27.5	235	13	Q8FV6 Q8FV6 brachydanio
7	356	25.7	68	6	Q9N139 Q9N139 bos taurus
8	264.5	19.1	143	13	Q9193 Q9193 xenopus lae
9	255	18.4	142	13	Q9193 Q9193 xenopus lae
10	220	15.9	275	11	Q80MWS Q80MWS mus musculi
11	218	15.7	318	13	Q7T2H3 Q7T2H3 oncorhynch
12	206	14.9	276	13	Q9DD2 Q9DD2 gallus gall
13	203.5	14.8	483	13	Q800K7 Q800K7 paratichthy
14	201	14.5	289	11	Q8K2X6 Q8K2X6 mus musculi
15	199.5	14.4	267	6	O02764 O02764 cryctolagus
16	198.5	14.3	283	6	Q9XSZ8 Q9XSZ8 cercoptithec

17	194.5	14.0	438	13	Q9DFV0 Q9DFV0 brachydanio
18	182.5	13.9	159	11	Q9YKE0 Q9YKE0 ractus novy
19	182.5	13.2	459	11	Q62327 Q62327 mus musculi
20	181.5	13.1	320	12	O57091 O57091 ectromelia
21	181.5	13.1	330	12	O57300 O57300 ectromelia
22	181.5	13.1	320	12	Q7TDM8 Q7TDM8 ectromelia
23	179	12.9	482	11	Q88734 Q88734 mus musculi
24	178.5	12.9	189	6	O97530 O97530 canis fami
25	178.5	12.9	316	12	O57092 O57092 ectromelia
26	178	12.8	651	13	Q98SM6 Q98SM6 gallus gall
27	177.5	12.8	446	6	Q95ND3 Q95ND3 felis silve
28	177.5	12.8	1101	5	Q964D2 Q964D2 entamoeba h
29	176.5	12.7	467	13	Q80010 Q80010 gallus gall
30	175.5	12.7	167	12	O72762 O72762 cowpox viru
31	175.5	12.7	1074	5	Q964D1 Q964D1 entamoeba h
32	174	12.5	223	4	O86Y5 O86Y5 homo sapien
33	173	12.5	305	13	Q800K8 Q800K8 paratichthy
34	171	12.3	285	13	Q9DGH7 Q9DGH7 gallus gall
35	170.5	12.3	167	12	Q9DUL2 Q9DUL2 cowpox viru
36	169	12.2	462	13	Q805B0 Q805B0 gallus gall
37	168.5	12.1	167	12	Q8UYL3 Q8UYL3 vaccinia vi
38	168.5	12.1	186	13	Q7ZZY5 Q7ZZY5 gallus gall
39	168.5	12.1	433	11	Q91ZM6 Q91ZM6 ractus novy
40	168.5	12.1	474	11	O86Y6 O86Y6 ractus novy
41	166.5	12.0	189	6	Q95185 Q95185 felis silve
42	166.5	12.0	278	6	Q8SQ34 Q8SQ34 sus scrofa
43	165.5	11.9	319	6	Q9TV79 Q9TV79 cryctolagus
44	165.5	11.9	320	12	O57079 O57079 cowpox viru
45	164.5	11.9	263	6	Q9XS60 Q9XS60 cryctolagus

## ALIGNMENTS

RESULT 1	PRELIMINARY;	PRT;	427 AA.
ID Q8CFT3			
AC Q8CFT3			
DT 01-MAR-2003 (TEMBLrel. 23, Created)			
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)			
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)			
DE Similar to nerve growth factor receptor.			
GN NGFR.			
OS Mus musculus (Mouse).			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Eumleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX NCBI_TaxID=10090;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Eye;			
RA Strauberg R.;			
RT Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.			
DR EMBL: BC038365; AA038365.1; -.			
DR MGD; MGI:97323; NGFR.			
DR GO; GO:0005035; F:death receptor activity; IDA.			
DR GO; GO:0005515; F:protein binding; IPI.			
DR GO; GO:0007417; P:central nervous system development; IMP.			
DR GO; GO:0006917; P:induction of apoptosis; IDA.			
DR InterPro: IPR000489; Death			
DR InterPro: IPR006209; EGF-like			
DR InterPro: IPR008262; Lipase_AS			
DR InterPro: IPR001368; TNFR_cf			
DR Pfam; PFO0531; death; 1.			
DR Pfam; PFO0020; TNFR_cf; 4.			
DR SMART; SM00005; DEATH; 1.			
DR SMART; SM00208; TNFR; 4.			
DR PROSITE; PSS0017; DEATH_DOMAIN; 1.			
DR PROSITE; PS0186; EGF_2; 1.			
DR PROSITE; PS00120; LIPASE_SER; 1.			
DR PROSITE; PS00652; TNFR_NGFR_1; 3.			
DR PROSITE; PSS0050; TNFR_NGFR_2; 4.			
DR Receptor.			

SEQUENCE 427 AA; 45647 MW; 7AC73263F7B31436 CRC64;  
Query Match 93.5%; Score 1297; DB 11; Length 427;  
Best Local Similarity 92.9%; Pred. No. 5.1e-116;  
Matches 235; Conservative 6; Mismatches 10; Indels 2; Gaps 1;  
QY 1 MRAGAAGSAMDRL--LILLILLIGVSSGAKETCTGLYTHSGECKKCNLGEVGAOPC 58  
DB 1 MRAGAAGSAMDRLRILLILLILLIGVSSFGAKETCTGMYTHSGECKKCNLGEVGAOPC 60  
QY 59 GANQVTCBCLDNVTSDVVSATBPCKPCTECGLQSMSPCYEADDAVCRCAVGYODE 118  
DB 61 GANQVTCBCLDNVTSDVVSATBPCKPCTECGLQSMSPCYEADDAVCRCSYGYODE 120  
QY 119 ETGHCACGVCVCGSLVFCSCDKONTVCECECEGTYSDEANHVDPCLPCTVCEDETEROL 178  
DB 121 ETGRCACGVCVCGSLVFCSCDKONTVCECECEGTYSDEANHVDPCLPCTVCEDETEROL 180  
QY 179 RECTPWADAECEBIPGRWIPRSTPPEGSSTAPSTOEPEVPEODLVPSVTADMTTWG 238  
DB 181 RECTPWADAECEBIPGRWITRSTPPEGSSTAPSTOEPEVPEODLVPSVTADMTTWG 240  
QY 239 SSQPVYTRGTDN 251  
DB 241 SSQPVYTRGTADN 253  
RESULT 2  
Q8BY1 PRELIMINARY; PRT; 417 AA.  
AC Q8BY1;  
DT 01-MAR-2003 (TREMblrel. 23, Created)  
DT 01-OCT-2003 (TREMblrel. 25, Last sequence update)  
DE Tumor necrosis factor receptor 16.  
GN NGFR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Skin;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium.  
RT the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
DR EMBL; AK037248; BAC29775.1; -.  
DR MGD; MGI:97323; NGFR.  
DR GO; GO:0005035; P:death receptor activity; IDA.  
DR GO; GO:0005515; P:protein binding; IPI.  
DR GO; GO:0007411; P:axon guidance; IMP.  
DR GO; GO:0007417; P:central nervous system development; IMP.  
DR GO; GO:0006917; P:induction of apoptosis; IDA.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR008262; Lipase AS.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PR00531; death\_1.  
DR Pfam; PR00020; TNFR\_c6; 4.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00208; TNFR; 4.  
DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS00120; LIPASE\_SER; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 4.  
SQ SEQUENCE 417 AA; 44672 MW; CD0440EF7E70A617 CRC64;  
Query Match 89.9%; Score 1247; DB 11; Length 417;  
Best Local Similarity 92.6%; Pred. No. 3.1e-111;

Matches 225; Conservative 6; Mismatches 10; Indels 2; Gaps 1;  
QY 11 MDRLR--LILLILLIGVSSGAKETCTGLYTHSGECKKCNLGEVGAOPCGANQVTCBPC 68  
DB 1 MDRLRLLLLLLLLLIGVSSFGAKETCTGMYTHSGECKKCNLGEVGAOPCGANQVTCBPC 60  
QY 69 LDNVPFSDVVSATBPCKPCTECGLQSMSPCYEADDAVCRCAVGYODEBTHCAVSY 128  
DB 61 LDNVPFSDVVSATBPCKPCTECGLQSMSPCYEADDAVCRCSYGYODEBTHCAVSY 120  
QY 129 CEGVSGVLFSCQDKONTVCECECEGTYSDEANHVDPCLPCTVCEDETEROLRECTPWADAE 188  
DB 121 CEGVSGVLFSCQDKONTVCECECEGTYSDEANHVDPCLPCTVCEDETEROLRECTPWADAE 180  
QY 189 CEELPGRWIPRSTPPEGSSTAPSTOEPEVPEODLVPSVTADMTTWGSSQPVYTRGT 248  
DB 181 CEELPGRWITRSTPPEGSSTAPSTOEPEVPEODLVPSVTADMTTWGSSQPVYTRGT 240  
QY 249 TDN 251  
DB 241 ADN 243  
RESULT 3  
Q9PRG7 PRELIMINARY; PRT; 401 AA.  
AC Q9PRG7;  
DT 01-MAY-2000 (TREMblrel. 13, Created)  
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)  
DE p75 neurotrophin receptor A-2.  
GN p75NTRA.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxId=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hutson L.D., Richards A.P., Bothwell M.;  
RT "Life and death in the developing Xenopus retina: The role of the p75  
neurotrophin receptor.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBS databases.  
DR EMBL; AF172400; AAD51031.1; -.  
DR HSP; P07174; INGR.  
DR GO; GO:0004872; P:receptor activity; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PR00531; death\_1.  
DR Pfam; PR00020; TNFR\_c6; 4.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00208; TNFR; 4.  
DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
KM Receptor  
SQ SEQUENCE 401 AA; 43419 MW; D13BCA7863BEECF CRC64;  
Query Match 44.7%; Score 619.5; DB 13; Length 401;  
Best Local Similarity 48.7%; Pred. No. 4.1e-51;  
Matches 116; Conservative 32; Mismatches 73; Indels 17; Gaps 5;  
QY 18 LILLIGVSS--GGAKETCTGLYTHSGECKKCNLGEVGAOPCGANQVTCBCLDNVTSS 75  
DB 5 LFIILGCMATLNAQKPCPSGQYTTAKGSCISQVVEGVYKRGVQVTCBCLDNVTSS 64  
QY 76 DVVSATBPCKPCTECGLQSMSPCYEADDAVCRCAVGYODEBTHCAVSYCEAGVCEVSGSL 135  
DB 65 DTLSHTACKPCTECGKHMEAPCVESDDAVCAVGYFTDKKSGQCTLCKSCPEGFM 124